GenCore version 5.1.6
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OM nucleic – nucleic search, using sw model

Run on: June 25, 2004, 06:11:13 ; Search time 4270.53 Seconds
                                          (without alignments)
                                          13027.239 Million cell updates/sec

Title: US-10-054-680-3
Perfect score: 1863
Sequence: 1 atggcgtggttaaggttgca..........ggaaagccagtattgggtga 1863

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1:   em_estba:*
                 2:   em_esthum:*
                 3:   em_estin:*
                 4:   em_estmu:*
                 5:   em_estov:*
                 6:   em_estpl:*
                 7:   em_estro:*
                 8:   em_htc:*
                 9:   gb_est1:*
                 10: gb_est2:*
                 11: gb_htc:*
                 12: gb_est3:*
                 13: gb_est4:*
                 14: gb_est5:*
                 15: em_estfun:*
                 16: em_estom:*
                 17: em_gss_hum:*
                 18: em_gss_inv:*
                 19: em_gss_pln:*
                 20: em_gss_vrt:*
                 21: em_gss_fun:*
                 22: em_gss_mam:*
                 23: em_gss_mus:*
                 24: em_gss_pro:*
                 25: em_gss_rod:*
                 26: em_gss_phg:*
                 27: em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1784.4	95.8	1788	29	AY401283	AY401283 Homo sapi
	2	1783	95.7	3186	11	BC036783	BC036783 Homo sapi
	3	1739.4	93.4	1788	29	AY401284	AY401284 Pan trogl
	4	1544.4	82.9	1788	29	AY401285	AY401285 Mus muscu
	5	1521	81.6	2534	11	AK044636	AK044636 Mus muscu
	6	971	52.1	1589	11	CNSLT1IBJ	BX248763 human ful
	7	899.6	48.3	941	13	BX374548	BX374548 BX374548
	8	805	43.2	887	12	BI913344	BI913344 603178823
	9	784.8	42.1	2922	29	AY398961	AY398961 Homo sapi
	10	768.2	41.2	939	13	BX347210	BX347210 BX347210
	11	755	40.5	2922	29	AY398963	AY398963 Mus muscu
	12	739.8	39.7	792	12	BI522813	BI522813 603175911
	13	737.8	39.6	920	13	BX368185	BX368185 BX368185
	14	710.4	38.1	4374	11	AK035163	AK035163 Mus muscu
	15	708.4	38.0	922	13	BX390204	BX390204 BX390204
	16	673.2	36.1	775	13	BQ770745	BQ770745 UI-M-FIO-
	17	638	34.2	3573	11	AK048160	AK048160 Mus muscu
	18	635.4	34.1	2516	29	AY408693	AY408693 Homo sapi
	19	607	32.6	2881	29	AY398962	AY398962 Pan trogl
	20	598.6	32.1	971	13	BX368184	BX368184 BX368184
	21	574.6	30.8	752	14	CF532853	CF532853 UI-M-GHO-
c	22	553.6	29.7	1062	29	CNS04DXR	AL286344 Tetraodon
	23	503.8	27.0	588	14	CF533347	CF533347 UI-M-FYO-
	24	497	26.7	704	14	CF729293	CF729293 UI-M-HDO-
	25	483.2	25.9	854	13	BX325851	BX325851 BX325851
	26	456.8	24.5	676	10	BB280958	BB280958 BB280958
	27	412.4	22.1	503	28	BZ211245	BZ211245 CH230-426
c	28	407.4	21.9	499	28	BH349372	BH349372 CH230-32M
	29	403.4	21.7	2515	29	AY408695	AY408695 Mus muscu
	30	397.2	21.3	911	13	BU901346	BU901346 AGENCOURT
	31	368.4	19.8	1201	13	BX355386	BX355386 BX355386
	32	363.6	19.5	829	29	CC501501	CC501501 CH240_339
	33	359	19.3	569	12	BI906774	BI906774 603064517
	34	352	18.9	741	14	CF539360	CF539360 UI-M-GHO-
	35	341.2	18.3	830	13	BU747974	BU747974 CH3#016_H
c	36	339.4	18.2	833	13	BU747973	BU747973 CH3#016_H
c	37	338	18.1	1020	29	CNS03Y28	AL265769 Tetraodon
	38	327.4	17.6	2472	29	AY408694	AY408694 Pan trogl
c	39	320	17.2	384	28	AZ258968	AZ258968 RPCI-23-1
c	40	304.4	16.3	818	28	BZ163286	BZ163286 CH230-276
	41	303	16.3	462	9	AL712986	AL712986 DKFZp686J
	42	295.8	15.9	693	10	BB648018	BB648018 BB648018
c	43	294.2	15.8	551	29	FR0052027	AL688306 Fugu rubr
	44	289.8	15.6	712	13	BY732330	BY732330 BY732330
	45	285.6	15.3	900	14	CF265737	CF265737 AGENCOURT

RESULT 1
AY401283

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LOCUS       AY401283               1788 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Homo sapiens SLC8A3 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY401283
VERSION     AY401283.1  GI:39757272
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1788)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
  PUBMED    14671302
REFERENCE   2  (bases 1 to 1788)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
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     source          1. .1788
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            <1. _.>1788
                     /gene="SLC8A3"
                     /locus_tag="HCM0839"
ORIGIN
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  Query Match            95.8%;   Score 1784.4;  DB 29;  Length 1788;
  Best Local Similarity  99.9%;   Pred. No. 0;
  Matches 1785;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps    0;
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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy     61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Qy    121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Db    121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy    181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db    181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy    241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db    241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300

Qy    301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy    361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy    421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Db    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540

Qy    541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Db    541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

Qy    601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Db    601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660

Qy    661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Db    661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

Qy    721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780

Qy    781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Db    781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840

Qy    841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Db    841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900

Qy    901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Db    901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Qy    961  AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020

Qy   1021  TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080

Qy   1081  ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Db   1081  ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140

Qy   1141  TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Db   1141  TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200

Qy   1201  GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGCTGTACTCCTGACAGTGGTGAGG 1260
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Db   1201  GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGCTGTACTCCTGACAGTGGTGAGG 1260

Qy   1261  AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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Qy   1321  AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Db   1321  AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

Qy   1381  CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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RESULT 2
BC036783
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LOCUS           BC036783               3186 bp    mRNA    linear   HTC 19-NOV-2003
DEFINITION      Homo sapiens solute carrier family 8 (sodium-calcium exchanger),
                member 3, mRNA (cDNA clone IMAGE:5732743), with apparent retained
                intron.
ACCESSION       BC036783
VERSION         BC036783.1  GI:23331089
KEYWORDS        HTC.
SOURCE          Homo sapiens (human)
  ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1  (bases 1 to 3186)
  AUTHORS       Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
                Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
                Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
                Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
                Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
                Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
                Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
                Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
                Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
                McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
                Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
                Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
                Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
                Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
                Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
                Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
                Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
                Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE         Generation and initial analysis of more than 15,000 full-length
                human and mouse cDNA sequences
  JOURNAL       Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE       22388257
  PUBMED        12477932
REFERENCE       2  (bases 1 to 3186)
  AUTHORS       Strausberg,R.
  TITLE         Direct Submission
  JOURNAL       Submitted (23-AUG-2002) National Institutes of Health, Mammalian
                Gene Collection (MGC), Cancer Genomics Office, National Cancer
                Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                USA
  REMARK        NIH-MGC Project URL: http://mgc.nci.nih.gov
  COMMENT       Contact: MGC help desk
                Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: Invitrogen
                cDNA Library Preparation: Life Technologies, Inc.
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: National Institutes of Health Intramural
                Sequencing Center (NISC),
                Gaithersburg, Maryland;
                Web site: http://www.nisc.nih.gov/
                Contact: nisc_mgc@nhgri.nih.gov
                Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
                Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
```

Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 79 Row: j Column: 21
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 17865803
This clone has the following problem: retained intron.

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FEATURES             Location/Qualifiers
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                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
ORIGIN
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  Matches 1812;  Conservative      0;  Mismatches    25;  Indels    4;  Gaps    1;

Qy         1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db       558 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 617

Qy        61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       618 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 677

Qy       121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       678 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 737

Qy       181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Db       858 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 917

Qy       361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       918 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 977
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Qy      421  CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      978  CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC  1037

Qy      481  ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC  540
             |||||||||||||||||||||||||||||.||||||||||||||||||||||||||||||
Db     1038  ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC  1097

Qy      541  ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1098  ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA  1157

Qy      601  CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||.
Db     1158  CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT  1217

Qy      661  CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1218  CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC  1277

Qy      721  TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1278  TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC  1337

Qy      781  ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC  840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1338  ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC  1397

Qy      841  CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC  900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1398  CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC  1457

Qy      901  CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1458  CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC  1517

Qy      961  AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1518  AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT  1577

Qy     1021  TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1578  TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT  1637

Qy     1081  ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC  1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1638  ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC  1697

Qy     1141  TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1698  TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT  1757

Qy     1201  GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1758  GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG  1817

Qy     1261  AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC  1320
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Db     1818 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1877

Qy     1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Db     1878 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1937

Qy     1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Db     1938 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1997

Qy     1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Db     1998 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 2057

Qy     1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Db     2058 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 2117

Qy     1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Db     2118 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 2177

Qy     1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2178 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 2237

Qy     1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2238 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2297

Qy     1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
                 ||||||||||||||||||||||||||||||||||||||||||    ||||| |  || |
Db     2298 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 2353

Qy     1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
                 |  |  || |  |||  ||||||||     |     ||||| 
Db     2354 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 2394
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RESULT 3
AY401284
LOCUS   AY401284   1788 bp   DNA   linear   GSS 15-DEC-2003
DEFINITION Pan troglodytes SLC8A3 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY401284
VERSION   AY401284.1 GI:39757273
KEYWORDS   GSS.
SOURCE   Pan troglodytes (chimpanzee)
  ORGANISM Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1 (bases 1 to 1788)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.

COMMENT   This sequence was made by sequencing genomic exons and ordering
           them based on alignment.
FEATURES   Location/Qualifiers
     source   1. .1788
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene   <1. .>1788
                     /gene="SLC8A3"
                     /locus_tag="HCM0839"
ORIGIN

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   Best Local Similarity 97.8%;   Pred. No. 0;
   Matches 1746; Conservative   0; Mismatches   40; Indels   0; Gaps   0;

Qy   1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy   61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
            ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TTTGTGCTCTTTCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy   121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy   181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy   241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCG 300

Qy   301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db   301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACGATTAAGAAACCCAATGGAGAA 360

Qy   361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db   361 ACCAGCACAACCACTATTCGAGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy   421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

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              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       421  CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC  480

Qy       481  ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC  540
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       481  ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC  540

Qy       541  ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA  600
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |    | | |
Db       541  ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCACCTA  600

Qy       601  CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT  660
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Db       601  CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT  660

Qy       661  CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC  720
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       661  CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC  720

Qy       721  TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC  780
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       721  TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC  780

Qy       781  ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC  840
              | | | | | | | | | | | | | | | | | | | | | | | | |   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       781  ATGCACAAAAAGTACCGCACAGATAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC  840

Qy       841  CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC  900
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Db       841  CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC  900

Qy       901  CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC  960
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       901  CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC  960

Qy       961  AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT  1020
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Db       961  AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCTAAT  1020

Qy      1021  TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT  1080
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |   | | | | | | | | | | | | | |
Db      1021  TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGGATCCAAGCCACTCGT  1080

Qy      1081  ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC  1140
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1081  ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC  1140

Qy      1141  TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT  1200
              | | | | | | | | | |    | | | | | | | | | | | | | | | | |    | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1141  TCCAGCATGANNGAGGTGCACACCGATGANNCTGAGGACTTTATTTCCAAGGTCTTCTTT  1200

Qy      1201  GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG  1260
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Db      1201  GACCCATGTTCTTACCAATGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG  1260

Qy      1261  AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC  1320
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |       | | |
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Db    1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTNNNGCC 1320

Qy    1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Db    1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

Qy    1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Db    1381 CAGAAGGAGTTCTCCGTAGGCATAATTNNNGACGACATTTNNNAGGAGGATGAACACTTN 1440

Qy    1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Db    1441 NNNNNAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGNCTCCA 1500

Qy    1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
           ||||||  |||||||      ||||||||||||||  |||||||||||||||||| ||||||
Db    1501 GCAATANNCAACAGTNNNNCCTTGCCTCGGGCTGTNNTAGCCTCCCCTTGTGTNGCCACA 1560

Qy    1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Db    1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620

Qy    1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680

Qy    1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy    1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
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RESULT 4
AY401285

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LOCUS       AY401285              1788 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Mus musculus SLC8A3 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY401285
VERSION     AY401285.1  GI:39757274
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1788)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
  PUBMED    14671302
REFERENCE   2  (bases 1 to 1788)
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AUTHORS    Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
           Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
           Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
           Adams,M.D. and Cargill,M.
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COMMENT    This sequence was made by sequencing genomic exons and ordering
           them based on alignment.
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ORIGIN
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Best Local Similarity    91.5%;  Pred. No. 0;
Matches 1635;  Conservative    0;  Mismatches  151;  Indels   0;  Gaps    0;
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Qy       1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db       1 ATGGCGTGGTTACGGCTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACT 60

Qy      61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Db      61 TTTGTGCTCTTCCTGAATTGTCTTCGAGCAGAGGCTGGTGACTCGGGGGATGTGCCCAGT 120

Qy     121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Db     121 GCAGGGCAGAACAATGAGTCCTGTTCGGGGTCATCAGACTGCAAGGAGGGTGTCATTTTG 180

Qy     181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
           |||||||||| || |||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CCAATCTGGTATCCAGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy     241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db     241 TTTGTGGCCCTGATATACATGTTTCTTGGGGTGTCTATCATTGCTGACCGATTCATGGCA 300

Qy     301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
           ||||||||||||| || || |||||||||| ||||| || ||||| |||||||||||||
Db     301 TCTATTGAAGTCATTACTTCCCAAGAGAGGGAAGTGACCATCAAGAAGCCCAATGGAGAG 360

Qy     361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
           |||||||||| || ||||||||| |||||||||||||||||||| ||||||||| ||||||
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Qy     421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db     421 CTGGGCTCTTCTGCTCCAGAGATTCTCCTGTCTTTAATTGAGGTGTGTGGTCACGGGTTC 480

Qy     481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Db     481 ATTGCTGGTGATCTGGGACCATCTACCATCGTTGGCAGTGCAGCCTTCAACATGTTCATC 540

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Qy     661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Qy     721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Db     721 TTTCCCGTGTGTGTCCTGCTGGCTTGGGTGGCAGATAAGCGACTGCTCTTCTACAAATAC 780

Qy     781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Qy     841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Qy     901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
           |     ||  ||||||| ||||| || ||||| || ||||| || ||||||||||||||
Db     901 TTTACACCTTTGGAAGGAAAGGAGGTAGATGAATCTCGCAGGGAAATGATCCGGATTCTA 960

Qy     961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
           |||||||||| ||||||||||||||| |||||| |||||||||||||||||||||||||||
Db     961 AAGGATCTGAAACAAAAACACCCAGAAAAGGACCTAGATCAGCTGGTGGAGATGGCCAAT 1020

Qy    1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Db    1021 TACTATGCTCTTTCCCATCAACAGAAGAGCCGTGCTTTCTACCGCATCCAAGCCACCCGG 1080

Qy    1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Db    1081 ATGATGACTGGTGCGGGCAATATACTTAAGAAGCATGCAGCCGAGCAAGCCAAGAAGACC 1140

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Qy    1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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Qy    1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Db    1321 AATGCAGGGGCAGACTATGAGTTCACAGAGGGCACTGTGGTTCTGAAGCCAGGAGAGACC 1380
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Qy    1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440.
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Qy    1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Qy    1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Qy    1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
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RESULT 5
AK044636
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LOCUS       AK044636                2534 bp    mRNA    linear    HTC 20-SEP-2003
DEFINITION  Mus musculus adult retina cDNA, RIKEN full-length enriched library,
            clone:A930029A02 product:solute carrier family 8 (sodium/calcium
            exchanger), member 3, full insert sequence.
ACCESSION   AK044636
VERSION     AK044636.1  GI:26336660
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
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REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
              Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
              Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
              Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
              Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
              Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
              Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
              sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
              FANTOM Consortium.
  TITLE   Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
              Group Phase I & II Team.
  TITLE   Analysis of the mouse transcriptome based on functional annotation
              of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6 (bases 1 to 2534)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
              Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
              Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
              Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
              Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
              Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
              Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
              Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
              Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
              Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
              Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
              Muramatsu,M. and Hayashizaki,Y.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
              Physical and Chemical Research (RIKEN), Laboratory for Genome
              Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
              RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
              Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
              URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
              Fax:81-45-503-9216)
  COMMENT   cDNA library was prepared and sequenced in Mouse Genome
              Encyclopedia Project of Genome Exploration Research Group in Riken
              Genomic Sciences Center and Genome Science Laboratory in RIKEN.
              Division of Experimental Animal Research in Riken contributed to
              prepare mouse tissues.
              Retina RNA was provided by Dr. Stefano Gustincich (Department of
              Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA
              02115, USA) whose assistance is gratefully acknowledged. Please
              visit our web site for further details.
              URL:http://genome.gsc.riken.go.jp/
              URL:http://fantom.gsc.riken.go.jp/.
FEATURES   Location/Qualifiers

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CDS             713. .>2533
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                RREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILK
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ORIGIN
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Query Match              81.6%;   Score 1521;   DB 11;   Length 2534;
Best Local Similarity    90.2%;   Pred. No. 0;
Matches 1662;  Conservative    0;  Mismatches  175;  Indels   6;  Gaps    3;


Qy         1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGG-CTGGTTAC 59
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Db       603 ATGGCGTGGTTACGGCTGCACCCTCTCACCTCTGCCTTCCTCCATCTTGGGCCTGGTTAC 662


Qy        60 CTTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAG 119
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Qy       120 CACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCT 179
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Db       723 TGCAGGGCAGAACAATGAGTCCTGTTCGGGGTCATCAGACTGCAAGGAGGGTGTCATTTT 782


Qy       180 GCCAA-TCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCT 238
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Db       783 GCCAACTCTGGTATCCAGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCT 842


Qy       239 ATTTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGG 298
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Db       843 ATTTTGTGGCCCTGATATACATGTTTCTTGGGGTGTCTATCATTGCTGACCGATTCATGG 902


Qy       299 CATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAG 358
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Db          903  CATCTATTGAAGTCATTACTTCCCAAGAGAGGGAAGTGACCATCAAGAAGCCCAATGGAG  962

Qy          359  AAACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGG  418
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Qy          419  CCCTGGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGT  478
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Qy          479  TCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCA  538
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Qy          539  TCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATC  598
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Qy          599  TACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGA  658
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Qy          659  TTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCT  718
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Qy          719  TCTTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAAT  778
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Qy          779  ACATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTG  838
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Qy          839  ACCACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGA  898
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Qy          899  ACCTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTC  958
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Qy          959  TCAAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCA  1018
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Qy    1559 CAGTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTC 1618
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Qy    1679 GTACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACT 1738
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Db    2399 AGGGTTAAAATAGTAGATGAGGAGGAGTACGAGAGGCAAGAGA 2441


RESULT 6
CNSLT1IBJ
LOCUS       CNSLT1IBJ             1589 bp    mRNA    linear    HTC 18-JUN-2003
DEFINITION  human full-length cDNA 5-PRIME end of clone CS0DB006YD18 of
            Neuroblastoma of Homo sapiens (human).
ACCESSION   BX248763
VERSION     BX248763.1  GI:28375580
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 1589)
  AUTHORS    Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE      Full-length cDNA libraries and normalization
  JOURNAL    Unpublished
  REMARK     Contact : Feng Liang Email : fliang@lifetech.com URL :
             http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
             Faraday Avenue
REFERENCE    2  (bases 1 to 1589)
  AUTHORS    Genoscope.
  TITLE      Direct Submission
  JOURNAL    Submitted (13-FEB-2003) Genoscope - Centre National de Sequencage :
             BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
             - Web : www.genoscope.cns.fr)
COMMENT      1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
             end enriched, double-strand cDNA was digested with Not I and cloned
             into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library
             was normalized. Library was constructed by Life Technologies, a
             division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1589
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DB006YD18"
                     /tissue_type="Neuroblastoma"
                     /note="end : 5-PRIME~Cot 10-normalized~vector pCMVSPORT_6"
     CDS             619. .>1589
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAD66570.1"
                     /db_xref="GI:28375581"
                     /translation="MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQN
                     NESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASI
                     EVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGF
                     IAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLY
                     MILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIE
                     TEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRREMIRILKDL"
ORIGIN

   Query Match            52.1%;  Score 971;  DB 11;  Length 1589;
   Best Local Similarity   100.0%;  Pred. No. 2.7e-274;
   Matches  971;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


Qy        1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      619 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 678


Qy       61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      679 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 738


Qy      121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      739 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 798
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Qy    181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    799 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 858

Qy    241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    859 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 918

Qy    301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    919 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 978

Qy    361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    979 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 1038

Qy    421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1039 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 1098

Qy    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1099 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 1158

Qy    541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1159 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 1218

Qy    601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Db   1219 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1278

Qy    661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1279 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1338

Qy    721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Db   1339 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1398

Qy    781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1399 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 1458

Qy    841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1459 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 1518

Qy    901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1519 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1578

Qy    961 AAGGATCTGAA 971
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Db   1579 AAGGATCTGAA 1589
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RESULT 7
BX374548

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LOCUS          BX374548                941 bp     mRNA    linear   EST 08-MAY-2003
DEFINITION     BX374548 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
               cDNA clone CS0DB006YD18 5-PRIME, mRNA sequence.
ACCESSION      BX374548
VERSION        BX374548.1  GI:30438490
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
  ORGANISM     Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1  (bases 1 to 941)
  AUTHORS      Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE        Full-length cDNA libraries and normalization
  JOURNAL      Unpublished (2001)
COMMENT        Contact: Genoscope
               Genoscope - Centre National de Sequencage
               BP 191 91006 EVRY cedex - France
               Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
               Library was constructed by Life Technologies, a division of
               Invitrogen. This sequence belongs to sequence cluster 7256.r For
               more information about this cluster, see
               http://www.genoscope.cns.fr/
               cgi-bin/cluster.cgi?seq=CS0DB006DB09_DB1287_2&cluster=7256.r.
               Contact : Feng Liang Email : fliang@lifetech.com URL :
               http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
               Faraday Avenue Genoscope sequence ID : CS0DB006DB09_DB1287_2.
FEATURES             Location/Qualifiers
     source          1..941
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DB006YD18"
                     /tissue_type="NEUROBLASTOMA COT 10-NORMALIZED"
                     /clone_lib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
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  Query Match                48.3%;   Score 899.6;   DB 13;   Length 941;
  Best Local Similarity      97.7%;   Pred. No. 2.2e-253;
  Matches  919;  Conservative    0;  Mismatches   21;  Indels    1;  Gaps    1;
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Qy      685 GTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCC 744
            | ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        1 GGCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCC-GTGTGTGTCCTTCTGGCC 59


Qy      745 TGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGAC 804
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       60 TGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGAC 119


Qy      805 AAACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGAT 864
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      120 AAACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGAT 179
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Qy     865 GGGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGAA 924
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     180 GGGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGAA 239

Qy     925 GTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCA 984
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     240 GTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCA 299

Qy     985 GAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAACAG 1044
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     300 GAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAACAG 359

Qy    1045 AAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATC 1104
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     360 AAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATC 419

Qy    1105 CTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACC 1164
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     420 CTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACC 479

Qy    1165 GATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTG 1224
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     480 GATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTG 539

Qy    1225 GAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACC 1284
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Db     540 GAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACC 599

Qy    1285 ATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTC 1344
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Db     600 ATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTC 659

Qy    1345 ACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATA 1404
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Db     660 ACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATA 719

Qy    1405 ATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGC 1464
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Db     720 ATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGNTAGGTTGAGCAATGTCCGC 779

Qy    1465 ATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTG 1524
           |||||||||||||||||||||||||||||||||     |||||||||     | |||||
Db     780 ATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTNNCAGCATATTCAAACAGTCTTCCTTG 839

Qy    1525 CCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCAT 1584
           ||||||||||||||||||| ||||||| |||| |||||||||||||||||||||||||||
Db     840 CCTCGGGCTGTCCTAGCCTNCCCTTGNGTGGNCACAGTTACCATCTTGGATGATGACCAT 899

Qy    1585 GCAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAG 1625
           ||   |||||||||||||||||||||||||||||||||||
Db     900 GCNAGCATCTTCACTTTTGAATGTGATACTATTCATGTCAG 940


RESULT 8
BI913344
LOCUS         BI913344                887 bp    mRNA     linear   EST 16-OCT-2001
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DEFINITION   603178823F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5243308 5',
             mRNA sequence.
ACCESSION    BI913344
VERSION      BI913344.1  GI:16177710
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 887)
  AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
  TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL    Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Life Technologies, Inc.
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLAM11613  row: m  column: 05
             High quality sequence stop: 782.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5243308"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_121"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
ORIGIN

  Query Match             43.2%;  Score 805;  DB 12;  Length 887;
  Best Local Similarity   98.0%;  Pred. No. 1.8e-225;
  Matches  836;  Conservative    0;  Mismatches   15;  Indels    2;  Gaps    2;

Qy        916 GGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAA 975
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAA 60

Qy        976 AAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCC 1035
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCC 120

Qy       1036 CACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCA 1095
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCA 180

Qy       1096 GGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAG 1155
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAG 240

Qy       1156 GTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTAC 1215
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Db        241 GTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTAC 300

Qy       1216 CAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATG 1275
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Db        301 CAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATG 360

Qy       1276 TCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGAC 1335
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Db        361 TCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGAC 420

Qy       1336 TATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCC 1395
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Db        421 TATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCC 480

Qy       1396 GTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGC 1455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGC 540

Qy       1456 AATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGT 1515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGT 600

Qy       1516 CTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGAT 1575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGAT 660

Qy       1576 GATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATT 1635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        661 GATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTA-T 719

Qy       1636 GGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACAGTCATCGTCCCC 1695
          |||||  ||||||||||||||||||||||||||  |||||||||||||||||||||||||
Db        720 GGTGTAATGGAGGTCAAGGTTCTGCGGACATCATGTGCCCGGGGTACAGTCATCGTCCCC 779

Qy       1696 TTT-AGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGG 1754
          |||  |||||| |||||||||||||||||| ||     |  | |  |||||||| ||||||
Db        780 TTTCAGGACAGGAGAAGGGACAGCCAAGGCTGCACGCTAAGGACTTGAAGACCCATATGC 839

Qy       1755 GGAGTTGGAATTC 1767
          |||||||||||||
Db        840 GGAGTTGGAATTC 852
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RESULT 9
AY398961
LOCUS   AY398961   2922 bp   DNA   linear   GSS 15-DEC-2003
DEFINITION Homo sapiens SLC8A1 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.

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ACCESSION   AY398961
VERSION     AY398961.1  GI:39754950
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2922)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 2922)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
     gene            <1..>2922
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                     /locus_tag="HCM0065"
ORIGIN

  Query Match           42.1%;   Score 784.8;  DB 29;  Length 2922;
  Best Local Similarity 68.3%;   Pred. No. 3.8e-219;
  Matches 1165;  Conservative    0;  Mismatches  502;  Indels   39;  Gaps    4;


Qy      109 GACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAG 168
                || || || ||  ||| | | | ||     ||| | || ||||   |||| ||| |
Db      112 GAAATGGAAGGAGAAGGAAATGAAACTGGTGAATGTACTGGATCATATTACTGTAAGAAA 171


Qy      169 GGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGG 228
                || || || |||| || ||| | ||   |  ||||||| |||||||||| ||||| ||
Db      172 GGGGTGATTTTGCCCATTTGGGAACCCCAAGACCCTTCTTTTGGGGACAAAATTGCTAGA 231


Qy      229 GTCATTGTCTATTTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGAC 288
               |  | |||| |||||||||||| || |  ||||||||| ||||| || || ||||| |||||
Db      232 GCTACTGTGTATTTTGTGGCCATGGTCTACATGTTTCTTGGAGTCTCTATCATAGCTGAT 291


Qy      289 CGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAA 348
               || ||||||| | |||||| ||||||||||||||||| |||||||| |  | || || ||||||
Db      292 CGGTTCATGTCCTCTATAGAAGTCATCACATCTCAAGAAAAAGAAATAACCATAAAGAAA 351


Qy      349 CCCAATGGAGAAACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTG 408
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              ||||||||||| |||| || || ||| | || ||||||||||||||| || || |||||||
Db    352 CCCAATGGAGAGACCACCAAGACAACTGTGAGGATCTGGAATGAAACAGTTTCTAACCTG 411

Qy    409 ACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGT 468
              ||| | |||||||||| || ||||||||||||||| |||||| || ||||||||| ||||||
Db    412 ACCTTGATGGCCCTGGGATCTTCTGCTCCTGAGATTCTCCTTTCAGTAATTGAAGTGTGT 471

Qy    469 GGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTC 528
              || ||| |||| ||| || || || || ||| ||||| || || |||||| || |||
Db    472 GGCCATAACTTCACTGCAGGAGACCTCGGTCCTAGCACCATCGTGGGAAGTGCTGCATTC 531

Qy    529 AACATGTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAG 588
              || |||||||||| |||| ||||||| || ||| | || |||||||||| ·| |||
Db    532 AATATGTTCATCATTATTGCACTCTGTGTTTATGTGGTGCCTGACGGAGAGACAAGGAAG 591·

Qy    589 ATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGG 648
              || |||||| | || |||||||| | || || || |||||||||||| ||||
Db    592 ATTAAGCATTTGCGTGTCTTCTTTGTGACAGCAGCCTGGAGCATCTTTGCCTACACCTGG 651

Qy    649 CTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTC 708
              || || || ||| || | ||| | || |||||||| || |||| |||||||| | ||
Db    652 CTTTACATTATTTTGTCTGTCATATCTCCTGGTGTTGTGGAGGTCTGGGAAGGTTTGCTT 711

Qy    709 ACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTC 768
              ||| ||||||||||||| | ||||| | | || ||||| || |||| |||| ||
Db    712 ACTTTCTTCTTCTTTCCCATCTGTGTTGTGTTCGCTTGGGTAGCGGATAGGAGACTTCTG 771

Qy    769 TTCTACAAATACATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAG 828
              || ||||| || | |||| | ||| || | | ||| || | || || || || ||
Db    772 TTTTACAAGTATGTCTACAAGAGGTATCGAGCTGGCAAGCAGAGGGGGATGATTATTGAA 831

Qy    829 ACAGAGGGTGACCACCC---------TAAGGGCATTGAGATGGATGGGAAAATGATGAAT 879
              || || ||| || | | ||||| ||||| |||||| || | |||
Db    832 CATGAAGGAGACAGGCCATCTTCTAAGACTGAAATTGAAATGGACGGGAAAGTGGTCAAT 891

Qy    880 TCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAG------------------ 921
              || ||| || | || | | |||| | ||
Db    892 TCTCATGTTGAAAATTTCTTAGATGGTGCTCTGGTTCTGGAGGTGGATGAGAGGGACCAA 951

Qy    922 GAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACAC 981
              || | || || | | |||| ||| |||||| ||||| || ||||| || ||
Db    952 GATGATGAAGAAGCTAGGCGAGAAATGGCTAGGATTCTGAAGGAACTTAAGCAGAAGCAT 1011

Qy    982 CCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAA 1041
              ||||| || || |||| || | | || | || || || ||| | | || || ||
Db   1012 CCAGATAAAGAAATAGAGCAATTAATAGAATTAGCTAACTACCAAGTCCTAAGTCAGCAG 1071

Qy   1042 CAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAAT 1101
              || ||| || | || || || || || |||||| ||||| | |||||||| || |||||
Db   1072 CAAAAAAGTAGAGCATTTTATCGCATTCAAGCTACTCGCCTCATGACTGGAGCTGGCAAC 1131

Qy   1102 ATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCAC 1161
              || | |||| ||||||||| || ||||| | ||||||| ||||||| |||||| ||
Db   1132 ATTTTAAAGAGGCATGCAGCTGACCAAGCAAGGAAGGCTGTCAGCATGCACGAGGTCAAC 1191

Qy   1162 ACCGATGAGCCTG---AGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAG 1218
              || || | | ||| | ||| | || ||| ||||||||| | | | | | || |||
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Db    1192 ACTGAAGTGACTGAAAATGACCCTGTTAGTAAGATCTTCTTTGAACAAGGGACATATCAG 1251

Qy    1219 TGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCA 1278
            || ||||||||||||| |||| ||| || | | | | ||| || || || |
Db    1252 TGTCTGGAGAACTGTGGTACTGTGGCCCTTACCATTATCCGCAGAGGTGGTGATTTGACT 1311

Qy    1279 AAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTAT 1338
            || || ||| ||| |||| || |||||||||| | || ||||| ||| |||| |||
Db    1312 AACACTGTGTTTGTTGACTTCAGAACAGAGGATGGCACAGCAAATGCTGGGTCTGATTAT 1371

Qy    1339 GAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTG 1398
            || || || || || || || ||||| | |||||| || || ||||||||| || |||
Db    1372 GAATTTACTGAAGGAACTGTGGTGTTTAAGCCTGGTGATACCCAGAAGGAAATCAGAGTG 1431

Qy    1399 GGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAAT 1458
            || || || ||||| || || ||||||||||||||||| | ||| |||| | ||||||
Db    1432 GGTATCATAGATGATGATATCTTTGAGGAGGATGAAAATTTCCTTGTGCATCTCAGCAAT 1491

Qy    1459 GTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTT 1518
            ||| || || |||| || || || | ||| || || |
Db    1492 GTCAAAGTATCTTCTGAAGCTTCAGAAGATGGCATACTGGAAGC---------CAATCAT 1542

Qy    1519 CCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGAT 1578
            | || | ||| ||| | || || | ||||| || || || || ||||||
Db    1543 GTTTCTACACTTGCTTGCCTCGGATCTCCCTCCACTGCCACTGTAACTATTTTTGATGAT 1602

Qy    1579 GACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGT 1638
            ||||| ||||||||| || |||||||||||| | | ||||||| ||||||||| |||||
Db    1603 GACCACGCAGGCATTTTTACTTTTGAGGAACCTGTGACTCATGTGAGTGAGAGCATTGGC 1662

Qy    1639 GTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGGTACAGTCATCGTCCCCTTT 1698
            | |||||||| || || || | ||||| || || || || || | || ||||| || |
Db    1663 ATCATGGAGGTGAAAGTATTGAGAACATCTGGAGCTCGAGGAAATGTTATCGTTCCATAT 1722

Qy    1699 AGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAG 1758
            | || | ||||||||| |||| ||||| || |||||| ||||| ||||| | ||| |||
Db    1723 AAAACCATCGAAGGGACTGCCAGAGGTGGAGGGGGAGGATTTTGAGGACACTTGTGGAGAG 1782

Qy    1759 TTGGAATTCAAGAATGATGAAACTGT 1784
            | ||||||| ||||||||||| |||
Db    1783 CTCGAATTCCAGAATGATGAAATTGT 1808
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RESULT 10
BX347210
LOCUS   BX347210   939 bp   mRNA   linear   EST 05-MAY-2003
DEFINITION BX347210 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
            cDNA clone CS0DB006YD18 5-PRIME, mRNA sequence.
ACCESSION   BX347210
VERSION   BX347210.1 GI:30381158
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 939)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

```
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 7256.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0BAA004ZB09_CS00355_1&cluster=7256.r.
            Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0BAA004ZB09_CS00355_1.
FEATURES             Location/Qualifiers
     source          1. .939
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DB006YD18"
                     /tissue_type="NEUROBLASTOMA COT 10-NORMALIZED"
                     /clone_lib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

   Query Match              41.2%;  Score 768.2;  DB 13;  Length 939;
   Best Local Similarity    95.6%;  Pred. No. 1.4e-214;
   Matches  854;  Conservative    0;  Mismatches   33;  Indels   6;  Gaps    6;

Qy      105 AGGGGACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAA 164
            |||||||||||| |||||||||||||||||||||||||||||| |||||||||||||||||
Db       22 AGGGGACGTGCC-AGCACAGGGCAGAACAATGAGTCCTGTT-AGGGTCATCGGACTGCAA 79

Qy      165 GGAGGGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGC 224
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       80 GGAGGGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGC 139

Qy      225 CAGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGC 284
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      140 CAGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGC 199

Qy      285 TGACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAA 344
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      200 TGACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAA 259

Qy      345 GAAACCCAATGGAGAAACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAA 404
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      260 GAAACCCAATGGAGAAACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAA 319

Qy      405 CCTGACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGT 464
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      320 CCTGACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGT 379

Qy      465 GTGTGGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGC 524
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
.Db    380 GTGTGGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGC 439

Qy     525 CTTCAACATGTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCG 584
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     440 CTTCAACATGTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCG 499

Qy     585 CAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACAT 644
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     500 CAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACAT 559

Qy     645 CTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCT 704
              ||||||||||||||||||||||||||'|||||||||||||||||||||||||||| ||||||
Db     560 CTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGG-AGGCCT 618

Qy     705 CCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACT 764
              ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db     619 CCTCACTCTCTTCTTC-TTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACT 677

Qy     765 GCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCAT 824
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||   ||
Db     678 GCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACAAACACCGAGGGATTATAT 737

Qy     825 AGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCA 884
              |||||||||||||||||||||||| |||| ||| ||||| ||||||||| |||||||||||
Db     738 AGAGACAGAGGGTGACCACCCTAGGGGCTTTGGGATGGGTGGGAAAAGGATGAATTCCCA 797

Qy     885 TTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGT-CCCGCAGAG 943
              |||||||| |||||| | ||||||| ||||||||| ||||||||| | | ||||||||
Db     798 TTTTCTAGGAGGGAAACCTGTGCCCCCTGAAGGGAAGAAAGTGGATTAATCCCCGCAGAG 857

Qy     944 AGATGATCCGGATTCTC-AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTT 995
              ||||||  || |  ||||| |  ||||||||| |  |||| |||   |  || | |
Db     858 AGATGAACCCGGTTCTCTAGGGATCTGAAACCAAAAACCCCCCAAAAAGGCCT 910
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RESULT 11
AY398963

REFERENCE   2 (bases 1 to 2922)
    AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
               Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
               Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
               Adams,M.D. and Cargill,M.
    TITLE   Direct Submission
    JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
               Rockville, MD 20850, USA
    COMMENT   This sequence was made by sequencing genomic exons and ordering
               them based on alignment.
FEATURES   Location/Qualifiers
     source   1. .2922
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
     gene   <1. .>2922
                     /gene="SLC8A1"
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ORIGIN

     Query Match   40.5%;   Score 755; DB 29; Length 2922;
     Best Local Similarity   67.8%;   Pred. No. 2.3e-210;
     Matches 1134; Conservative   0; Mismatches 500; Indels   39; Gaps   4;

Qy   142 TGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTGCCAATCTGGTACCCGGAGAAC 201
            ||| | || |||| |||| ||| | || || ||| |||| || ||| | || | ||
Db   145 TGTACTGGCTCATATTACTGTAAGAAAGGGGTGATCTTGCCCATTTGGGAACCCCAAGAC 204

Qy   202 CCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATATACATG 261
            || || ||||||||||| |||||| ||||| || | | ||| ||||||||||| | | |||||||
Db   205 CCATCTTTTGGGGACAAAAATTGCTAGAGCAACTGTGTATTTTGTGGCCATGGTCTACATG 264

Qy   262 TTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATCACCTCT 321
            |||||||| || || || || ||||| ||||| || ||| | ||||| || |||||||||||||
Db   265 TTCCTTGGAGTTTCTATTATTGCAGACCGGTTTATGTCCTCTATAGAGGTCATCACCTCT 324

Qy   322 CAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACAACCACTATTCGG 381
            ||||||| || | || || || ||||||||| |||||||| |||| || || || | |
Db   325 CAAGAGAAAGAAATAACGATAAAGAAACCGAATGGAGAGACCACCAAGACGACGGTGAGA 384

Qy   382 GTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAG 441
            ||||||| || ||||| || |||||||||| | |||||||||||| || |||||||||||
Db   385 ATCTGGAACGAGACTGTGTCGAACCTGACCTTGATGGCCCTGGGATCTTCTGCTCCTGAG 444

Qy   442 ATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTCATTGCTGGTGATCTGGGACCT 501
            || ||||| || | ||||| ||||| || ||| |||| || || || || ||||| ||
Db   445 ATTCTCCTGTCAGTCATTGAAGTGTGCGGCCATAACTTCACCGCAGGGGACCTGGGTCCC 504

Qy   502 TCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATCATCATTGGCATCTGTGTCTAC 561
            ||||| || || |||||| ||||| |||||||||||||||||||||| || | ||||||| |||
Db   505 AGCACCATCGTGGGGAGTGCTGCCTTTAACATGTTCATCATAATCGCACTCTGTGTTTAC 564

Qy   562 GTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCT 621
            ||| |||| || ||||||||| |||| |||||||||||| || || ||||| | || ||
Db   565 GTGGTCCCTGATGGAGAGACAAGGAAGATCAAGCATCTGCGTGTGTTCTTTGTGACAGCA 624

Qy   622 GCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGT 681

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                    ||  ||||||  ||||||||||| |  ||||||| |||||| || | || | ||| ||| |||||
Db     625 GCCTGGAGCATCTTTGCCTATACCTGGCTTTATATAATCTTGTCTGTCAGCTCTCCTGGA 684

Qy     682 GTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTG 741
                    || || |||| |||||||||.| || ||| ||||||||||| | || || | |
Db     685 GTTGTGGAGGTCTGGGAAGGCTTGCTTACTTTCTTCTTCTTTCCCATCTGCGTTGTGTTC 744

Qy     742 GCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACA 801
                    || ||||| |||||| |  || || |||||| |||||| || |  |||| |||| | |
Db     745 GCGTGGGTAGCAGACAGGCGGCTTCTCTTTTACAAGTATGTCTACAAGCGGTACAGGGCC 804

Qy     802 GACAAACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCC---------TAAGGGC 852
                    | ||| || | || || |||||| ||    || || ||| ||       |  |
Db     805 GGCAAGCAGAGGGGGATGATCATTGAACATGAAGGAGACAGACCAGCTTCCAAAACTGAA 864

Qy     853 ATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTG 912
                    || || ||||||||||| || | || || ||| ||        ||          | | |||
Db     865 ATCGAAATGGATGGGAAAGTGGTCAACTCTCATGTTGACAATTTCTTAGATGGGGCTCTG 924

Qy     913 G------------------AAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGG 954
                    |                         |  | ||| | || || || |  | |||||| ||
Db     925 GTTTTGGAAGTTGATGAGAGGGACCAAGATGATGAGGAAGCCAGGCGTGAGATGGCAAGG 984

Qy     955 ATTCTCAAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATG 1014
                    ||||| ||||| || |||||| || || || |||||| || | || || | | || |
Db     985 ATTCTGAAGGAACTTAAGCAGAAGCATCCTGAGAAAGAAATTGAGCAATTAATAGAATTA 1044

Qy     1015 GCCAATTACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCC 1074
                    ||||| ||| | |  || || || ||||| ||||| || || ||| | || |||||
Db     1045 GCCAACTACCAGGTCCTAAGTCAACAGCAGAAAAGCCGAGCATTTTACAGGATTCAAGCT 1104

Qy     1075 ACTCGTATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAG 1134
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Db     1105 ACTCGCCTGATGACCGGAGCTGGCAACATCTTGAAGAGGCACGCAGCTGATCAAGCAAGG 1164

Qy     1135 AAGGCCTCCAGCATGAGCGAGGTGCACACCGATGAGCCTG---AGGACTTTATTTCCAAG 1191
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Db     1165 AAGGCTGTCAGTATGCATGAAGTCAACATGGAAATGGCTGAAAACGACCCAGTCAGTAAG 1224

Qy     1192 GTCTTCTTTGACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACA 1251
                    |||||||||| | | |  | ||||||||| || ||||||||||| |||| ||| ||
Db     1225 ATCTTCTTTGAGCAAGGAACATACCAGTGTCTAGAGAACTGTGGTACTGTGGCCCTCACC 1284

Qy     1252 GTGGTGAGGAAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGAT 1311
                    | || | | |||||| ||| || |  | || ||| ||| |||| || |||||| ||
Db     1285 ATTATGCGCAGAGGGGGCGACTTGAGCACCACTGTGTTTGTTGACTTCAGGACAGAAGAC 1344

Qy     1312 GGTTCTGCCAATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCA 1371
                    || | | |||||||| ||| |||| ||||| ||||| || || || || | ||| ||| |||
Db     1345 GGCACAGCCAATGCTGGGTCTGATTATGAATTCACGGAAGGGACTGTGATCTTCAAACCA 1404

Qy     1372 GGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGAT 1431
                    || |||||||||||||| || | || ||||| ||||||||| || || |||||| || |||
Db     1405 GGGGAGACCCAGAAGGAAATCAGAGTTGGCATCATTGATGATGATATCTTTGAAGAAGAT 1464

Qy     1432 GAACACTTCTTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGG 1491
                    ||| ||||| |||| | ||||||||||| | |  || |||| || ||
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Db      1465 GAAAACTTCCTTGTGCATCTTAGCAATGTCAGAGTCTCTTCAGATGTTTCAGAAGATGGC 1524

Qy      1492 ATGCCTCCAGCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGT 1551
                ||       | ||      || ||   | |    |     ||| || | || || |
Db      1525 AT---------ACTAGAATCCAATCACGCTTCTTCAATTGCTTGTCTTGGGTCACCCAGC 1575

Qy      1552 GTGGCCACAGTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGAT 1611
                ||||| | |||||| || ||||||||||||||||||||||||||| || |||||
Db      1576 ACTGCCACCATAACCATTTTTGATGATGACCATGCAGGCATCTTTACATTTGAGGAACCC 1635

Qy      1612 ACTATTCATGTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGT 1671
                | ||| || || ||||| ||||| | |||||||| |||||| || | || || ||
Db      1636 GTGACTCACGTGAGCGAGAGCATTGGCATCATGGAGGTGAAGGTTTTGAGAACCTCTGGA 1695

Qy      1672 GCCCGGGGTACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGT 1731
                || || || |   || ||| | |||| |  ||  | ||||| ||||||   ||||| ||
Db      1696 GCTCGAGGAAATGTTATCATTCCCTACAAAACTATTGAAGGCACAGCCCGAGGTGGAGGG 1755

Qy      1732 GAGGACTTTGAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGT 1784
                || ||||||||| |||||  | |||  ||| | ||||||| |||| |||||||  ||
Db      1756 GAAGACTTTGAGGACACCTGTGGAGAGCTCGAATTCCAGAACGATGAAATAGT 1808


RESULT 12
BI522813
LOCUS           BI522813                 792 bp    mRNA       linear   EST 29-AUG-2001
DEFINITION      603175911F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240066 5',
                mRNA sequence.
ACCESSION       BI522813
VERSION         BI522813.1  GI:15347605
KEYWORDS        EST.
SOURCE          Homo sapiens (human)
  ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1  (bases 1 to 792)
  AUTHORS       NIH-MGC http://mgc.nci.nih.gov/.
  TITLE         National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL       Unpublished (1999)
COMMENT         Contact: Robert Strausberg, Ph.D.
                Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: Life Technologies, Inc.
                 cDNA Library Preparation: Life Technologies, Inc.
                 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                 DNA Sequencing by: Incyte Genomics, Inc.
                 Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: LLAM11605  row: f  column: 03
                High quality sequence stop: 778.
FEATURES             Location/Qualifiers
     source          1. .792
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240066"
                     /lab_host="DH10B"
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ORIGIN

Query Match   39.7%; Score 739.8; DB 12; Length 792;
Best Local Similarity 98.7%; Pred. No. 2.9e-206;
Matches 767; Conservative   0; Mismatches   7; Indels   3; Gaps   2;

Qy   993 CTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAACAGAAGAGCCG 1052
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAACAGAAGAGCCG 60

Qy   1053 CGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCCTGAAGAA 1112
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCCTGAAGAA 120

Qy   1113 ACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCGATGAGCC 1172
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCGATGAGCC 180

Qy   1173 TGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGGAGAACTG 1232
           ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGGAGAACTG 240

Qy   1233 TGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCATGTATGT 1292
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCATGTATGT 300

Qy   1293 GGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCACAGAGGG 1352
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCACAGAGGG 360

Qy   1353 CACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAATTGATGA 1412
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAATTGATGA 420

Qy   1413 CGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCATAGAGGA 1472
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCATAGAGGA 480

Qy   1473 GGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGCCTCGGGC 1532
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGCCTCGGGC 540

Qy   1533 TGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATGCAGGCAT 1592
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATGCAGGCAT 600

```
Qy    1593 CTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGTGTTATGGAGGTCAA 1652
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 CTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGTGTTATGGAGGTCAA 660

Qy    1653 GGTTCTGCGGACATCAGGTGCCCGGGG-TACAGTCATCGTCCCCTTTAGGACAGTAGAAG 1711
           ||||||||||||||||||||||| ||||| ||||||||||||||||||||||||||||||
Db     661 GGTTCTGCGGACATCAGGTGCACGGGGCTACAGTCATCGTCCCCTTTAGGACAGTAGAAG 720

Qy    1712 GGACAGCCAAGGGTGGCGGT--GAGGACTTTGAAGACACATATGGGGAGTTGGAATT 1766
           ||||||||||||||||||||     ||||| ||||||||||||||||||||| | | |
Db     721 GGACAGCCAAGGGTGGCGGTCGACGGACTCTGAAGACACATATGGGGAGTTTGGAAT 777
```

RESULT 13
BX368185
```
LOCUS        BX368185                920 bp    mRNA    linear   EST 08-MAY-2003
DEFINITION   BX368185 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
             cDNA clone CS0DD006YJ07 5-PRIME, mRNA sequence.
ACCESSION    BX368185
VERSION      BX368185.1  GI:30445119
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 920)
  AUTHORS    Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE      Full-length cDNA libraries and normalization
  JOURNAL    Unpublished (2001)
COMMENT      Contact: Genoscope
             Genoscope - Centre National de Sequencage
             BP 191 91006 EVRY cedex - France
             Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
             Library was constructed by Life Technologies, a division of
             Invitrogen. This sequence belongs to sequence cluster 7256.r For
             more information about this cluster, see
             http://www.genoscope.cns.fr/
             cgi-bin/cluster.cgi?seq=CS0BAA006ZD07_CS00533_2&cluster=7256.r.
             Contact : Feng Liang Email : fliang@lifetech.com URL :
             http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
             Faraday Avenue Genoscope sequence ID : CS0BAA006ZD07_CS00533_2.
FEATURES             Location/Qualifiers
     source          1. .920
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DD006YJ07"
                     /tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
                     /clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
```

Query Match   39.6%;   Score 737.8; DB 13;   Length 920;
Best Local Similarity 95.1%;   Pred. No. 1.3e-205;

Matches 827; Conservative 0; Mismatches 33; Indels 10; Gaps 6;

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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     50 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 109

Qy     61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    110 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 169

Qy    121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    170 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 229

Qy    181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    230 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 289

Qy    241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    290 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 349

Qy    301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    350 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 409

Qy    361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    410 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 469

Qy    421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    470 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 529

Qy    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    530 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 589

Qy    541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    590 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 649

Qy    601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    650 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 709

Qy    661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||| |||
Db    710 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCT-CTCACTCTCTTTTTC 768

Qy    721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
           ||||||||||||||||||||||||||||||||||||||| |||||||| | || ||| |
Db    769 -TTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGAT-AACGACTGGTTTTTACCAA--TC 824

Qy    781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
          |||| ||||||||| ||| ||||||| ||| | ||| || | ||| | | |     |
Db    825 ATGCCCAAAAAGTCCCG-ACAGACCAACCCGNGGGATTT----TCTAGAGACCGAGGTGC 879
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Qy    841 CACCCTAAGGGCATTGAGATGGATGGGAAA 870
          |  ||  ||||| ||| |||||  || |||
Db    880 CCACCCTAGGGCCTTGGGATGGTGGGAAAA 909
```

RESULT 14
AK035163
LOCUS   AK035163   4374 bp   mRNA   linear   HTC 18-SEP-2003
DEFINITION Mus musculus 12 days embryo embryonic body between diaphragm region
            and neck cDNA, RIKEN full-length enriched library, clone:9430095C22
            product:SODIUM/CALCIUM EXCHANGER 2 PRECURSOR (NA(+)/CA(2+)-EXCHANGE
            PROTEIN 2) homolog [Rattus norvegicus], full insert sequence.
ACCESSION   AK035163
VERSION   AK035163.1 GI:26084435
KEYWORDS   HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE   High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE   Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE   Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
```

REFERENCE    6   (bases 1 to 4374)
  AUTHORS    Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
             Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
             Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
             Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
             Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
             Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
             Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
             Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
             Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
             Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
             Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
             Muramatsu,M. and Hayashizaki,Y.
  TITLE      Direct Submission
  JOURNAL    Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
             Physical and Chemical Research (RIKEN), Laboratory for Genome
             Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
             RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
             Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
             URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
             Fax:81-45-503-9216)
  COMMENT    cDNA library was prepared and sequenced in Mouse Genome
             Encyclopedia Project of Genome Exploration Research Group in Riken
             Genomic Sciences Center and Genome Science Laboratory in RIKEN.
             Division of Experimental Animal Research in Riken contributed to
             prepare mouse tissues.
             Please visit our web site for further details.
             URL:http://genome.gsc.riken.go.jp/
             URL:http://fantom.gsc.riken.go.jp/.
FEATURES             Location/Qualifiers
     source          1. .4374
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:9430095C22"
                     /db_xref="MGI:2399390"
                     /db_xref="taxon:10090"
                     /clone="9430095C22"
                     /tissue_type="embryonic body between diaphragm region and
                     neck"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="12 days embryo"
     misc_feature    281. .3046
                     /note="SODIUM/CALCIUM EXCHANGER 2 PRECURSOR
                     (NA(+)/CA(2+)-EXCHANGE PROTEIN 2) homolog [Rattus
                     norvegicus] (SWISSPROT|P48768, evidence: FASTY, 97%ID,
                     100%length, match=2763)
                     putative"
ORIGIN

  Query Match              38.1%;   Score 710.4;   DB 11;   Length 4374;
  Best Local Similarity    65.9%;   Pred. No. 4.5e-197;
  Matches 1092;  Conservative    0;  Mismatches  536;  Indels   30;  Gaps     3;

Qy        136 GAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTGCCAATCTGGTACCCG 195
              ||    |||    ||| || |      ||||| |     ||||| | ||||| | ||| | ||

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Db     401 GAAGGCTGCCAAGGTTCCTACCGCTGCCAACCAGGTGTGCTGCTGCCTGTGTGGGAACCC 460

Qy     196 GAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATA 255
           ||| |||| || || || |||||| |||| ||| | | || || |||||||||| || |
Db     461 GAGGACCCATCGCTGGGCGACAAGGTTGCACGGGCCGTGGTGTACTTTGTGGCCATGGTC 520

Qy     256 TACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATC 315
           |||||||||| || |||||| ||||||||| || || || |||||||| ||||| ||||||
Db     521 TACATGTTCCTGGGTGTGTCTATCATTGCCGATCGATTTATGGCATCCATTGAGGTCATC 580

Qy     316 ACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACAACCACT 375
           || || | |||| ||| | || || | || | |||||| || ||||||      |||
Db     581 ACATCCAAGGAGAAAGAGATCACCATCACCAAGGCAAATGGGGAGACCAGCGTGGGCACG 640

Qy     376 ATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCCTCTGCT 435
           | || ||||||| || || || ||||||| || || |||||||||||| |||| ||
Db     641 GTGCGCATCTGGAACGAGACGGTGTCCAACCTTACACTCATGGCCCTGGGCTCCTCAGCG 700

Qy     436 CCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTCATTGCTGGTGATCTG 495
           |||||||| || | || | || |||||| ||||| || ||| || |||||| ||
Db     701 CCTGAGATTCTGTTGACTGTCATCGAGGTCTGTGGCCACAACTTCCAGGCCGGTGAGCTA 760

Qy     496 GGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATCATCATTGGCATCTGT 555
           || || |||||| || || ||||| |||||||||||||||||||| | ||||||  | |||
Db     761 GGCCCAGGCACCATCGTGGGCAGTGCCGCCTTCAACATGTTTGTGGTCATTGCTGTTTGT 820

Qy     556 GTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATC 615
           || || || |||||| | || |||| || |||||||||||| || | ||||||||| ||
Db     821 GTGTATGTCATCCCGGCTGGCGAGAGCCGTAAGATCAAGCACCTGAGGGTCTTCTTTGTC 880

Qy     616 ACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCC 675
           || || | |||||| |||||||||||  ||||||| ||| | ||||| ||||| ||||||
Db     881 ACAGCCTCCTGGAGCATCTTTGCCTATGTCTGGCTTTATCTCATTCTAGCAGTTTTCTCC 940

Qy     676 CCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTC 735
           || ||||| |||||||| |||||  | || || |||||| || |||||| || ||||||||
Db     941 CCAGGTGTAGTCCAGGTGTGGGAGGCACTGCTCACACTGATCTTCTTCCCGGTGTGTGTG 1000

Qy     736 CTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTAC 795
           | | |||||| |||| || || || || |||||||||||||||||||||| || || ||||    |||
Db    1001 GTGTTTGCCTGGATGGCGGACAAGCGACTGCTCTTCTACAAGTACGTGTACAAGCGCTAC 1060

Qy     796 CGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATT 855
           ||||| ||| | | | |||||| |||||| | | |||||||| |||| || ||| ||||
Db    1061 CGCACCGACCCTCGCAGTGGAATCATCATCGGGGCAGAGGGAGACCCACCCAAGAGCATC 1120

Qy     856 GAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATG-----------GGAACCTG 903
           ||| ||||| || | | | || | | | | | |          | |
Db    1121 GAGCTGGACGGCACATTCGTGGGCACTGAGGTCCCTGGCGAGCTGGGCGCATTGGGCACA 1180

Qy     904 GTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAG 963
           | || || | | || | |||| ||| | ||| | |||| || || ||
Db    1181 GGTCCTGCTGAGGCGCGTGAACTAGATGCCAGCCGGCGTGAGGTCATCCAGATCCTTAAG 1240

Qy     964 GATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTAC 1023
           || ||||||| || |||||| || ||||||| | || ||||| ||| || |||||| |||
Db    1241 GACTTGAAGCAGAAGCACCCGGATAAGGACCTGGAGCAGCTGATGGGCATCGCCAAGTAC 1300
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Qy   1024 TATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATG 1083
          |||||  ||     |||||  |||||||||||||||||||||||  |||||  |||||  || ||
Db   1301 TATGCACTGCTGCACCAGCAGAAGAGCCGCGCCTTCTACCGCATCCAGGCCACGCGGCTG 1360

Qy   1084 ATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCC 1143
          |||||  |||||  ||||||  |  |||      |  |||||||  ||  ||      |||      ||   |      |
Db   1361 ATGACAGGTGCGGGCAATGTGCTGCGCAGACATGCTGCGGATGCTGCCCGCAGG---CCG 1417

Qy   1144 AGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGAC 1203
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Db   1418 GGAGCCACCGATGGTGCCCCCGATGATGAGGACGATGGTGCCAGTCGCATCTTCTTTGAG 1477

Qy   1204 CCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAA 1263
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Db   1478 CCCAGCCTCTATCACTGCCTGGAAAACTGCGGGTCAGTGCTGCTGTCCGTGGCTTGCCAG 1537

Qy   1264 GGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAAT 1323
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Db   1538 GGCGGTGAGGGCAACAGCACCTTCTACGTGGACTACCGTACCGAGGACGGTTCTGCAAAG 1597

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Db   1598 GCAGGCTCCGATTATGAGTACAGCGAGGGCACGCTGGTGTTCAAGCCCGGGGAGACGCAG 1657

Qy   1384 AAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTT 1443
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Db   1658 AAGGACCTGCGCATCGGGATCATCGACGACGACATCTTCGAGGAGGATGAGCACTTCTTC 1717

Qy   1444 GTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCA 1503
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Db   1718 GTGAGGCTGCTGAACCTGCGTGTGGGCGATGCTCAGGGCATGTTCGAG----------- 1765

Qy   1504 ATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTT 1563
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Db   1766 ---CCCGACGGCGGTGGGCGGCCCAAGGGGCGGCTGGTGGCGCCGCTGCTGGCCACTGTC 1822

Qy   1564 ACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCATGTC 1623
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Qy   1624 AGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACA 1683
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Db   1883 AGCGAGTGCATGGGCACTGTGGATGTGCGCGTGGTTCGCAGCTCGGGCGCCCGTGGCACT 1942

Qy   1684 GTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAA 1743
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Db   1943 GTACGCCTCCCCTACCGCACAGTGGACGGCACGGCCCGTGGCGGTGGTGTACATTACGAG 2002

Qy   1744 GACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC 1781
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Db   2003 GATGCTTGTGGAGAGCTGGAGTTCGGCGATGATGAGAC 2040
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RESULT 15
BX390204
LOCUS   BX390204   922 bp   mRNA   linear   EST 08-MAY-2003

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DEFINITION    BX390204 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
              cDNA clone CS0DD006YJ07 5-PRIME, mRNA sequence.
ACCESSION     BX390204
VERSION       BX390204.1  GI:30461412
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
  ORGANISM    Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1  (bases 1 to 922)
  AUTHORS     Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE       Full-length cDNA libraries and normalization
  JOURNAL     Unpublished (2001)
COMMENT       Contact: Genoscope
              Genoscope - Centre National de Sequencage
              BP 191 91006 EVRY cedex - France
              Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
              Library was constructed by Life Technologies, a division of
              Invitrogen. This sequence belongs to sequence cluster 7256.r For
              more information about this cluster, see
              http://www.genoscope.cns.fr/
              cgi-bin/cluster.cgi?seq=CS0BAG010ZA11_CS00945_1&cluster=7256.r.
              Contact : Feng Liang Email : fliang@lifetech.com URL :
              http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
              Faraday Avenue Genoscope sequence ID : CS0BAG010ZA11_CS00945_1.
FEATURES             Location/Qualifiers
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                     /tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
                     /clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

   Query Match              38.0%;  Score 708.4;  DB 13;  Length 922;
   Best Local Similarity    91.9%;  Pred. No. 6e-197;
     Matches 847;  Conservative    0;  Mismatches    66;  Indels    9;  Gaps    9;

Qy       30 CTCTGCCTTCCTCCATTTTGGGCTGGTTACCTTTGTGCTCTTCCTGAATGGTCTTCGAGC 89
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Db        3 CTCTGCCTTCCTCC-TTTTGGGCTGGTTACCTTTGTGCTCTTCCTG-ATGGTCTTCGAGC 60

Qy       90 AGAGGCTGGTGGCTCAGGGGACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTTCAGG 149
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Db       61 AGAGGCTGGTGGCTCAGGGGACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTTCAGG 120

Qy      150 GTCATCGGACTGCAAGGAGGGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCT 209
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Db      121 GTCATCGGACTGCAAGGAGGGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCT 180

Qy      210 TGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCCTTGG 269
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Db    181 TGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCCTTGG 240

Qy    270 GGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAG 329
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Qy    330 GGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACAACCACTATTCGGGTCTGGAA 389
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Qy    390 TGAAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATACTCCT 449
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Qy    450 CTCTTTAATTGAGGTGTGTGGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTACCAT 509
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Db    421 CTCTTTAATTGAGGTGTGTGGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTACCAT 480

Qy    510 TGTAGGGAGTGCAGCCTTCAACATGTTCATCATCATTGGCATCTGTGTCTACGTGATCCC 569
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TGTAGGGAGTGCAGCCTTCAACATGTTCATCATCATTGGCATCTGTGTCTACGTGATCCC 540

Qy    570 AGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAG 629
          |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db    541 AGACGGAGAGACTCGCAAGATCAAGCATTTACGAGTCTTCTTCATCACCGCTGCTTGGAG 600

Qy    630 TATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCA 689
          ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db    601 TATCTTTGCCTACATCTGGCTCTATATGATTCTGCCAGTCTTCTCCCCTGGTGTGGTCCA 660

Qy    690 GGTTT-GGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTG-TCCTTCTGGCCTGG 747
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Qy    748 GTGGCAG-ATAAACGACTGCT-CTTCTACAAATACATGCACAAAAAGTACCGCACAGACA 805
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Db    721 GTGGCAGTATAACCGACTGCTCCTTTTACAAATACATGCACATTAATGTCCGCACAGACA 780

Qy    806 AACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATG 865
          | |||||| || | | |||| ||||| |  | || ||||||| |||||| |||||| || ||
Db    781 ACCACCG-GGCACTTTCATTGAGACTGTCGTTG-CCACCCTTAGGGCACTGAGA-GGTTG 837

Qy    866 GGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGAAG 925
          || |||||||||| |||| ||   ||  ||  ||    |||| | | | || ||| |
Db    838 GGCAAATGATGATTTCCACTTCCTTATTTGTATCCCTGCGCCTCTTTAAGGCAAAGAAGA 897

Qy    926 TGGATGAGTCCCGCAGAGAGAT 947
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Db    898 CGTACCATCTCTCCCGTCAGTT 919
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Search completed: June 25, 2004, 15:31:20
Job time : 4276.53 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2004, 04:06:20 ; Search time 7009.69 Seconds
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                                           11519.487 Million cell updates/sec

Title: US-10-054-680-3
Perfect score: 1863
Sequence: 1 atggcgtggttaaggttgca..........ggaaagccagtattgggtga 1863

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1863	100.0	1863	6	AX496813	AX496813 Sequence
	2	1861.4	99.9	5146	9	AF510503	AF510503 Homo sapi
	3	1784.6	95.8	2766	6	AX496811	AX496811 Sequence
	4	1784.6	95.8	3812	6	AX496815	AX496815 Sequence
	5	1784.4	95.8	2534	9	HSNCX22	X93017 Homo sapien
	6	1783	95.7	2781	6	AX299471	AX299471 Sequence
	7	1783	95.7	2782	6	AX476818	AX476818 Sequence
	8	1783	95.7	2837	9	HSA304853	AJ304853 Homo sapi
	9	1783	95.7	2966	6	AX480881	AX480881 Sequence
	10	1783	95.7	5250	9	AF510501	AF510501 Homo sapi
	11	1783	95.7	5268	9	AF510502	AF510502 Homo sapi
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c	18	1544.4	82.9	183707	10	AC124384	AC124384 Mus muscu
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	21	1527	82.0	4854	10	RNU53420	U53420 Rattus norv
	22	1526.8	82.0	247722	2	AC099080	AC099080 Rattus no
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	28	805.2	43.2	3199	4	DOGSNCE	M57523 Dog cardiac
	29	799.4	42.9	3150	4	CATSCE	L35846 Felis catus
	30	796.2	42.7	3292	4	OCU52665	U52665 Oryctolagus
	31	795	42.7	1920	4	FCNCX1S4	U67075 Felis catus
	32	792.8	42.6	1832	9	AF109888	AF109888 Macaca mu
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41    784.4   42.1    6023     9   HSM808447         BX648299 Homo sapi
42    783.4   42.1    3168    10   CPU04955          U04955 Cavia porce
43    765.8   41.1    2805    10   AF109163          AF109163 Rattus no
44    765.8   41.1    3037    10   RNSCEA1           X68812 R.norvegicu
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ALIGNMENTS

RESULT 1
AX496813
LOCUS   AX496813   1863 bp   DNA   linear   PAT 26-SEP-2002
DEFINITION   Sequence 3 from Patent WO02059316.
ACCESSION   AX496813
VERSION   AX496813.1 GI:23342336
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hilbun,E. and Friddle,C.J.
  TITLE   Human ion exchanger proteins and polynucleotides encoding the same
  JOURNAL   Patent: WO 02059316-A 3 01-AUG-2002;
             LEXICON GENETICS INC (US)
FEATURES   Location/Qualifiers
     source   1. .1863
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ORIGIN

  Query Match   100.0%; Score 1863; DB 6; Length 1863;
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  Matches 1863; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy   61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Qy   121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Qy   181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Qy      241  TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA  300
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Qy      301  TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA  360
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Qy      361  ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC  420
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Qy      421  CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC  480
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Db      421  CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC  480

Qy      481  ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC  540
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Db      481  ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC  540

Qy      541  ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA  600
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Db      541  ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA  600

Qy      601  CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT  660
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Db      601  CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT  660

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Db      721  TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC  780

Qy      781  ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC  840
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Db      781  ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC  840

Qy      841  CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC  900
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Db      841  CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC  900

Qy      901  CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC  960
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Qy      961  AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT  1020
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Db      961  AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT  1020

Qy      1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT  1080
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Db    1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080

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Qy    1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Db    1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200

Qy    1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGCTGTACTCCTGACAGTGGTGAGG 1260
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Db    1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGCTGTACTCCTGACAGTGGTGAGG 1260

Qy    1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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Db    1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320

Qy    1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Db    1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

Qy    1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Db    1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440

Qy    1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Qy    1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Qy    1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Qy    1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Qy    1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Qy    1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
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Qy    1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGG 1860
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Db    1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGG 1860

Qy    1861 TGA 1863
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Db    1861 TGA 1863
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RESULT 2
AF510503
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LOCUS       AF510503                5146 bp    mRNA    linear   PRI 30-OCT-2002
DEFINITION  Homo sapiens Na+/Ca2+ exchanger isoform 3 splice variant 4 (SLC8A3)
            mRNA, complete cds; alternatively spliced.
ACCESSION   AF510503
VERSION     AF510503.1  GI:24421224
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 5146)
  AUTHORS   Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.
  TITLE     The human SLC8A3 gene and the tissue-specific Na(+)/Ca(2+)
            exchanger 3 isoforms
  JOURNAL   Gene 298 (1), 1-7 (2002)
  MEDLINE   22294016
   PUBMED   12406570
REFERENCE   2  (bases 1 to 5146)
  AUTHORS   Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-MAY-2002) Department of Biology, Unv. of Padova, via
            G. Colombo, Padova, PD 35131, Italy
FEATURES             Location/Qualifiers
     source          1..5146
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                     /map="14q24.2"
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     5'UTR           1..754
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                     /gene="SLC8A3"
                     /note="NCX3.4; expressed in skeletal muscle; alternatively
                     spliced"
                     /codon_start=1
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                     /db_xref="GI:24421225"
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                     IAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLY
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                     LVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE
                     DFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTE
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                     PRAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPF
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ORIGIN

   Query Match              99.9%;  Score 1861.4;  DB 9;  Length 5146;
   Best Local Similarity    99.9%;  Pred. No. 0;
   Matches 1862;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;


Qy        1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db      755 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 814

Qy       61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      815 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 874

Qy      121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Db      875 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 934

Qy      181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db      935 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 994

Qy      241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db      995 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 1054

Qy      301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1055 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 1114

Qy      361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Db     1115 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 1174

Qy      421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db     1175 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 1234

Qy      481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Db     1235 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 1294

Qy      541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Db     1295 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 1354

Qy      601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1355 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1414

Qy      661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1415 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1474
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Qy      721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC  780
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Db     1475 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1534

Qy      781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC  840
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Db     1535 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 1594

Qy      841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC  900
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Db     1595 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 1654

Qy      901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC  960
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Db     1655 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1714

Qy      961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Db     1715 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1774

Qy     1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
            ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db     1775 TACTATGCTCTTTCCCACCAACAGAAGAGCCGTGCCTTCTACCGTATCCAAGCCACTCGT 1834

Qy     1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Db     1835 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1894

Qy     1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Db     1895 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1954

Qy     1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
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Db     1955 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 2014

Qy     1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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Db     2015 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 2074

Qy     1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Qy     1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Qy     1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Qy     1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Qy     1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Db     2315  GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT  2374

Qy     1621  GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT  1680
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Db     2375  GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT  2434

Qy     1681  ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT  1740
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Qy     1741  GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA  1800
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Db     2495  GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA  2554

Qy     1801  GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGG  1860
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Db     2555  GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGG  2614

Qy     1861  TGA  1863
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Db     2615  TGA  2617
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RESULT 3
AX496811
LOCUS   AX496811   2766 bp   DNA   linear   PAT 26-SEP-2002
DEFINITION Sequence 1 from Patent WO02059316.
ACCESSION   AX496811
VERSION   AX496811.1 GI:23342335
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hilbun,E. and Friddle,C.J.
  TITLE   Human ion exchanger proteins and polynucleotides encoding the same
  JOURNAL   Patent: WO 02059316-A 1 01-AUG-2002;
            LEXICON GENETICS INC (US)
FEATURES   Location/Qualifiers
     source   1. .2766
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ORIGIN

  Query Match   95.8%;   Score 1784.6;   DB 6;   Length 2766;
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Qy       1  ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC  60
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Db       1  ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC  60

Qy      61  TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC  120
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Db     61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy    121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Qy    361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Qy    421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Qy    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Db    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540

Qy    541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Db    721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780

Qy    781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Db    781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840

Qy    841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Db    841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900

Qy    901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Qy    961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Db    961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020

Qy   1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080

Qy   1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Qy   1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Db   1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200

Qy   1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
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Db   1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260

Qy   1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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Db   1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320

Qy   1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Db   1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

Qy   1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Db   1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440

Qy   1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

Qy   1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Qy   1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Qy   1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
          |||||||||||||||||||||||||||||||||||||||||    ||||| |   || |
Db   1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1796
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Qy       1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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Db       1797 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837
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RESULT 4
AX496815
LOCUS   AX496815   3812 bp   DNA   linear   PAT 26-SEP-2002
DEFINITION   Sequence 5 from Patent WO02059316.
ACCESSION   AX496815
VERSION   AX496815.1 GI:23342337
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hilbun,E. and Friddle,C.J.
  TITLE   Human ion exchanger proteins and polynucleotides encoding the same
  JOURNAL   Patent: WO 02059316-A 5 01-AUG-2002;
             LEXICON GENETICS INC (US)
FEATURES   Location/Qualifiers
     source   1. .3812
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

   Query Match   95.8%;   Score 1784.6;   DB 6;   Length 3812;
   Best Local Similarity   98.5%;   Pred. No. 0;
   Matches 1813;   Conservative   0;   Mismatches   24;   Indels   4;   Gaps   1;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        618 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 677

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Db        678 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 737

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        738 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 797

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        798 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 857

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db        858 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 917

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        918 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 977

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Db        978    ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 1037

Qy        421    CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db       1038    CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 1097

Qy        481    ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Db       1098    ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 1157

Qy        541    ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1158    ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 1217

Qy        601    CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Db       1218    CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1277

Qy        661    CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Db       1278    CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1337

Qy        721    TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Db       1338    TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1397

Qy        781    ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Db       1398    ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 1457

Qy        841    CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Db       1458    CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 1517

Qy        901    CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Db       1518    CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1577

Qy        961    AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Db       1578    AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1637

Qy       1021    TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1638    TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1697

Qy       1081    ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Db       1698    ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1757

Qy       1141    TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Db       1758    TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1817

Qy       1201    GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
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Db      1818  GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG  1877

Qy      1261  AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC  1320
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Db      1878  AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC  1937

Qy      1321  AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC  1380
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Db      1938  AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC  1997

Qy      1381  CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC  1440
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Db      1998  CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC  2057

Qy      1441  TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA  1500
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Db      2058  TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA  2117

Qy      1501  GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA  1560
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Db      2118  GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA  2177

Qy      1561  GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT  1620
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Db      2178  GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT  2237

Qy      1621  GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT  1680
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Db      2238  GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT  2297

Qy      1681  ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT  1740
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Db      2298  ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT  2357

Qy      1741  GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA  1800
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Db      2358  GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG  2413

Qy      1801  GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA  1841
              | | |  || | ||| |||||||    |    |    |||||
Db      2414  GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA  2454


RESULT 5
HSNCX22
LOCUS        HSNCX22               2534 bp    DNA       linear    PRI 12-NOV-2000
DEFINITION   Homo sapiens partial SCL8A3 gene for solute carrier family 8
             (sodium/calcium exchanger), member 3 (SCL8A3), exon 2.
ACCESSION    X93017
VERSION      X93017.1  GI:1067133
KEYWORDS     SLC8A3 gene; sodium-calcium exchanger.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
  AUTHORS    Kraev,A., Chumakov,I. and Carafoli,E.
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COMMENT   Similar to X91213.
FEATURES   Location/Qualifiers
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     gene   281. .2126
                     /gene="SLC8A3"
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                     exchanger), member 3"
                     /number=2
ORIGIN

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     Matches 1785; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db   343 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 402

Qy   61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   403 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 462

Qy   121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   463 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 522

Qy   181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db   523 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 582

Qy   241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db   583 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 642

Qy   301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

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Db      643 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 702

Qy      361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Db      703 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 762

Qy      421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db      763 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 822

Qy      481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      823 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 882

Qy      541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Db      883 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 942

Qy      601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Db      943 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1002

Qy      661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Db     1003 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1062

Qy      721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Db     1063 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1122

Qy      781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Db     1123 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 1182

Qy      841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Db     1183 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 1242

Qy      901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1243 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1302

Qy      961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1303 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1362

Qy     1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Db     1363 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1422

Qy     1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Db     1423 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1482

Qy     1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Db      1483 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1542

Qy      1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1543 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1602

Qy      1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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Qy      1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Qy      1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Db      1783 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1842

Qy      1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Db      1903 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1962

Qy      1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Db      1963 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 2022

Qy      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2023 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2082

Qy      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
             ||||||||||||||||||||||||||||||||||||||||||| |
Db      2083 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGT 2128
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RESULT 6
AX299471
LOCUS   AX299471   2781 bp   DNA   linear   PAT 26-NOV-2001
DEFINITION   Sequence 1 from Patent WO0183744.
ACCESSION   AX299471
VERSION   AX299471.1 GI:17129228
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Wilm,C.
  TITLE   Natrium-calcium exchanger protein

FEATURES   Location/Qualifiers
     source   1. .2781
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"
     CDS   1. .>2781
                      /note="unnamed protein product"
                      /codon_start=1
                      /protein_id="CAD12716.1"
                      /db_xref="GI:17129229"
                      /db_xref="REMTREMBL:CAD12716"
                      /translation="MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQN
                      NESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASI
                      EVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGF
                      IAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLY
                      MILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIE
                      TEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRREMIRILKDLKQKHPEKDLDQ
                      LVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE
                      DFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTE
                      GTVVLKPGETQKEFSVGIIDDDIFEEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPL
                      PRAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPF
                      RTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRVKIVDEEEYERQENFFIALGEPKWM
                      ERGISGVRFFKDVTDRKLTMEEEEAKRIAEMGKPVLGEHPKLEVIIEESYEFKTTVDK
                      LIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFDYVMHFLTVFWK
                      VLFACVPPTEYCHGWACFAVSILIIGMLTAIIGDLASHFGCTIGLKDSVTAVVFVAFG
                      TSVPDTFASKAAALQDVYADASIGNVTGSNAVNVFLGIGLAWSVAAIYWALQGQEFHV
                      SAGTLAFSVTLFTIFAFVCISVLLYRRRPHLGGELGGPRGCKLATTWLFVSLWLLYIL
                      FATLEAYCYIKGF"
ORIGIN

     Query Match   95.7%;   Score 1783;   DB 6;   Length 2781;
     Best Local Similarity 98.4%;   Pred. No. 0;
     Matches 1812; Conservative   0; Mismatches   25;   Indels   4;   Gaps   1;

Qy   1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy   61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy   121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy   181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy   241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300

Qy   301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

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             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy    361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy    421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540

Qy    541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Db    541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

Qy    601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660

Qy    661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

Qy    721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Db    721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780

Qy    781 ATGCACAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Db    781 ATGCACAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840

Qy    841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Db    841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900

Qy    901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960

Qy    961 AAGGATCTGAAGCAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 AAGGATCTGAAGCAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020

Qy   1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
             |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db   1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGTGCCTTCTACCGTATCCAAGCCACTCGT 1080

Qy   1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140

Qy   1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Db        1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200

Qy        1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260

Qy        1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320

Qy        1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

Qy        1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Db        1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440

Qy        1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

Qy        1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Db        1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560

Qy        1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Qy        1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Db        1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680

Qy        1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Db        1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy        1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
               |||||||||||||||||||||||||||||||||||||||||||||||    ||||| |  || |
Db        1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1796

Qy        1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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Db        1797 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837
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RESULT 7
AX476818
LOCUS   AX476818   2782 bp   DNA   linear   PAT 12-AUG-2002
DEFINITION Sequence 1 from Patent WO0233086.
ACCESSION   AX476818
VERSION   AX476818.1 GI:22216098
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

FEATURES   Location/Qualifiers
     source   1. .2782
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

   Query Match   95.7%; Score 1783; DB 6; Length 2782;
   Best Local Similarity   98.4%; Pred. No. 0;
   Matches 1812; Conservative   0; Mismatches   25; Indels   4; Gaps   1;

Qy   1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 69

Qy   61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   70 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 129

Qy   121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   130 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 189

Qy   181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   190 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 249

Qy   241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db   250 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 309

Qy   301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Db   310 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 369

Qy   . 361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   370 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 429

Qy   421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   430 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 489

Qy   481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   490 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 549

Qy   541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db    550  ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA  609

Qy    601  CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    610  CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT  669

Qy    661  CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    670  CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC  729

Qy    721  TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    730  TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC  789

Qy    781  ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    790  ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC  849

Qy    841  CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    850  CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC  909

Qy    901  CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC  960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    910  CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATCCTC  969

Qy    961  AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    970  AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT  1029

Qy    1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1030 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT  1089

Qy    1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1090 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC  1149

Qy    1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT  1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1150 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT  1209

Qy    1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG  1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1210 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG  1269

Qy    1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC  1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1270 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC  1329

Qy    1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC  1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1330 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC  1389

Qy    1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC  1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1390 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC  1449
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Qy    1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1450 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1509

Qy    1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1510 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1569

Qy    1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1570 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1629

Qy    1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1630 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1689

Qy    1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1690 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1749

Qy    1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
           |||||||||||||||||||||||||||||||||||||||||    |||||| |  || |
Db    1750 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1805

Qy    1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
           | | |  || | ||| |||||||  |     |  |||||
Db    1806 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1846
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RESULT 8
HSA304853

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LOCUS       HSA304853               2837 bp    mRNA    linear   PRI 06-JUN-2001
DEFINITION  Homo sapiens mRNA for sodium/calcium exchanger, SCL8A3, alternative
            splice form B (SCL8A3 gene).
ACCESSION   AJ304853
VERSION     AJ304853.1  GI:14330384
KEYWORDS    alternative splicing; form B; SCL8A3 gene; SCL8A3 protein;
            Sodium/calcium exchanger.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gabellini,N.
  TITLE     Characterization of the human SCL8A3 gene for solute carrier family
            8, member 3 (sodium/calcium exchanger)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2837)
  AUTHORS   Bortoluzzi,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-DEC-2000) Bortoluzzi S., Department of Biology and
            Department of Biological Chemistry, University of Padova, via G.
            Colombo 3, 35131 PADOVA, ITALY
FEATURES             Location/Qualifiers
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RESULT 9
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DEFINITION  Sequence 41 from Patent WO0246415.
ACCESSION   AX480881
VERSION     AX480881.1  GI:22217538
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Query Match   95.7%; Score 1783; DB 6; Length 2966;
Best Local Similarity 98.4%; Pred. No. 0;
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RESULT 10
AF510501
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DEFINITION Homo sapiens Na+/Ca2+ exchanger isoform 3 splice variant 2 (SLC8A3)
            mRNA, complete cds; alternatively spliced.
ACCESSION   AF510501
VERSION   AF510501.1 GI:24421220
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 5250)
  AUTHORS   Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.
  TITLE   The human SLC8A3 gene and the tissue-specific Na(+)/Ca(2+)
            exchanger 3 isoforms
  JOURNAL   Gene 298 (1), 1-7 (2002)
  MEDLINE   22294016
   PUBMED   12406570

REFERENCE   2   (bases 1 to 5250)
    AUTHORS   Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.
    TITLE   Direct Submission
    JOURNAL   Submitted (09-MAY-2002) Department of Biology, Unv. of Padova, via
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ORIGIN

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Db     875  ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 934

Qy     181  CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db     935  CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 994

Qy     241  TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Qy      1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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RESULT 11
AF510502
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DEFINITION  Homo sapiens Na+/Ca2+ exchanger isoform 3 splice variant 3 (SLC8A3)
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ACCESSION   AF510502
VERSION     AF510502.1  GI:24421222
KEYWORDS    .
SOURCE      Homo sapiens (human)
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REFERENCE   1  (bases 1 to 5268)
  AUTHORS   Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.
  TITLE     The human SLC8A3 gene and the tissue-specific Na(+)/Ca(2+)
            exchanger 3 isoforms
  JOURNAL   Gene 298 (1), 1-7 (2002)
  MEDLINE   22294016
   PUBMED   12406570
REFERENCE   2  (bases 1 to 5268)
  AUTHORS   Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-MAY-2002) Department of Biology, Unv. of Padova, via
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  Query Match              95.7%;   Score 1783;   DB 9;   Length 5268;
  Best Local Similarity    98.4%;   Pred. No. 0;
  Matches 1812;  Conservative     0;  Mismatches    25;  Indels    4;  Gaps      1;


Qy           1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Qy          61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Db         815 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 874


Qy         121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Qy         421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db        1175 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 1234


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Qy    601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Db   1715 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1774

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Qy      1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Db      2315 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 2374

Qy      1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Qy      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
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Db      2495 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 2550

Qy      1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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Db      2551 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 2591
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RESULT 12
AX476820

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LOCUS       AX476820                126512 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 3 from Patent WO0233086.
ACCESSION   AX476820
VERSION     AX476820.1  GI:22216099
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Merkulov,G.V., Ketchum,K.A., Shao,W., Yan,C., di Francesco,V. and
            Beasley,E.M.
  TITLE     Isolated human transporter proteins, nucleic acid molecules
            encoding human transporter proteins, and uses thereof
  JOURNAL   Patent: WO 0233086-A 3 25-APR-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
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ORIGIN
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Query Match   95.7%; Score 1782.8; DB 6; Length 126512;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1784; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

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Db     2010 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 2069

Qy       61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Db     2070 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 2129

Qy      121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Db     2130 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 2189

Qy      181 CCAATCTGGTACCCGGAGAACCCTTCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db     2190 CCAATCTGGTACCCGGAGAACCCTTCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 2249

Qy      241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Qy      301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Db     2310 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 2369

Qy      361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Db     2370 ACCAGCACAACAACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 2429

Qy      421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db     2430 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 2489

Qy      481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Db     2490 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 2549

Qy      541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Db     2550 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 2609

Qy      601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Db     2610 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 2669

Qy      661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Qy      721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Db     2730 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 2789

Qy      781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Qy    841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC  900
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Qy    901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC  960
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Qy    961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Qy   1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Qy   1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Qy   1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
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Qy   1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Qy   1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Db   3390 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 3449

Qy   1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Qy    1741  GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
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RESULT 13
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LOCUS       AF508982              145118 bp    DNA     linear   PRI 24-OCT-2002
DEFINITION  Homo sapiens Na+/Ca2+ exchanger isoform 3 (SLC8A3) gene, promoter
            region and complete cds.
ACCESSION   AF508982
VERSION     AF508982.1  GI:22087482
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 145118)
  AUTHORS   Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.
  TITLE     The human SLC8A3 gene and the tissue-specific Na+/Ca2+ exchanger 3
            isoforms
  JOURNAL   Gene 298 (1), 1-7 (2002)
REFERENCE   2  (bases 1 to 145118)
  AUTHORS   Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.
  TITLE     Control of the Na+/Ca2+ exchanger 3 promoter by cAMP and Ca2+ in
            differentiating neurons
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 145118)
  AUTHORS   Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-MAY-2002) Department of Biology, University of
            Padova, via G. Colombo 3, Padova, PD 35131, Italy
FEATURES             Location/Qualifiers
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ORIGIN

   Query Match   95.7%;   Score 1782.8;   DB 9;   Length 145118;
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   Matches 1784; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Qy   61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Qy   181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db   21095 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 21154

Qy   241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db   21155 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 21214

Qy   301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

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Qy     361  ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC   420
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Qy     421  CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC   480
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Db   21335  CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC  21394

Qy     481  ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC   540
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Db   21395  ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC  21454

Qy     541  ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA   600
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Qy     601  CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT   660
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Db   21515  CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT  21574

Qy     661  CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC   720
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Db   21575  CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC  21634

Qy     721  TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC   780
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Db   21635  TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC  21694

Qy     781  ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC   840
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Qy     841  CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC   900
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Db   21755  CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC  21814

Qy     901  CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC   960
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Db   21815  CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC  21874

Qy     961  AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT  1020
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Db   22235 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 22294

Qy    1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Db   22295 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 22354

Qy    1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Db   22355 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 22414

Qy    1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Db   22415 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 22474

Qy    1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Db   22475 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 22534

Qy    1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Qy    1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   22595 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 22654

Qy    1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
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RESULT 14
AC009607
LOCUS   AC009607   146055 bp   DNA   linear   HTG 04-MAY-2001
DEFINITION Homo sapiens clone RP11-1I11, WORKING DRAFT SEQUENCE, 31 unordered
            pieces.
ACCESSION   AC009607
VERSION   AC009607.3 GI:8072446
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 146055)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.

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TITLE       Homo sapiens, clone RP11-1I11
JOURNAL     Unpublished
REFERENCE   2   (bases 1 to 146055)
AUTHORS     Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
            Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,
            Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A.,
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            Marquis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J.,
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            Naylor,J., Niloff,M., O'Connor,T., O'Donnell,P., Pavlin,B.,
            Peterson,K., Pollara,V., Riley,R., Roberts,D., Roy,A., Severy,P.,
            Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A.,
            Tesfaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A.,
            Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
TITLE       Direct Submission
JOURNAL     Submitted (28-AUG-1999) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On May 25, 2000 this sequence version replaced gi:7321520.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L1464
                Center clone name: 1_I_11
            -------------- Summary Statistics
                Sequencing vector: M13; M77815; 99% of reads
                Sequencing vector: Plasmid; n/a; %-0.f%% of reads
                0.776287932251235Chemistry: Dye-primer-amersham; 6% of reads
                Chemistry: Dye-terminator Big Dye; 94% of reads
                Assembly program: Phrap; version 0.960731
                Consensus quality: 126247 bases at least Q40
                Consensus quality: 134710 bases at least Q30
                Consensus quality: 138332 bases at least Q20
                Insert size: 160000; agarose-fp
                Insert size: 143055; sum-of-contigs
                Quality coverag.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 31 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     1166: contig of 1166 bp in length
            *     1167     1266: gap of 100 bp
            *     1267     2417: contig of 1151 bp in length
            *     2418     2517: gap of 100 bp
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*       2518       3635: contig of 1118 bp in length
*       3636       3735: gap of 100 bp
*       3736       4851: contig of 1116 bp in length
*       4852       4951: gap of 100 bp
*       4952       6701: contig of 1750 bp in length
*       6702       6801: gap of 100 bp
*       6802       8629: contig of 1828 bp in length
*       8630       8729: gap of 100 bp
*       8730      10482: contig of 1753 bp in length
*      10483      10582: gap of 100 bp
*      10583      12126: contig of 1544 bp in length
*      12127      12226: gap of 100 bp
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*      13932      16132: contig of 2201 bp in length
*      16133      16232: gap of 100 bp
*      16233      17951: contig of 1719 bp in length
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*      18052      20069: contig of 2018 bp in length
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*      20170      22565: contig of 2396 bp in length
*      22566      22665: gap of 100 bp
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*      24925      25024: gap of 100 bp
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*      26997      27096: gap of 100 bp
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*      33804      33903: gap of 100 bp
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*      38178      38277: gap of 100 bp
*      38278      42132: contig of 3855 bp in length
*      42133      42232: gap of 100 bp
*      42233      45874: contig of 3642 bp in length
*      45875      45974: gap of 100 bp
*      45975      50807: contig of 4833 bp in length
*      50808      50907: gap of 100 bp
*      50908      55690: contig of 4783 bp in length
*      55691      55790: gap of 100 bp
*      55791      60868: contig of 5078 bp in length
*      60869      60968: gap of 100 bp
*      60969      65180: contig of 4212 bp in length
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*      72596      79536: contig of 6941 bp in length
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*      79637      86013: contig of 6377 bp in length
*      86014      86113: gap of 100 bp
*      86114      98467: contig of 12354 bp in length
*      98468      98567: gap of 100 bp
*      98568     112312: contig of 13745 bp in length
*     112313     112412: gap of 100 bp
*     112413     128733: contig of 16321 bp in length
*     128734     128833: gap of 100 bp
*     128834     146055: contig of 17222 bp in length.
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                       /clone_lib="RPCI-11 Human Male BAC"
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     misc_feature      1267. .2417
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     misc_feature      3736. .4851
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     misc_feature      4952. .6701
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     misc_feature      6802. .8629
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     misc_feature      8730. .10482
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     misc_feature      12227. .13831
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     misc_feature      13932. .16132
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     misc_feature      16233. .17951
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     misc_feature      18052. .20069
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ORIGIN

   Query Match             95.7%;   Score 1782.8;   DB 2;   Length 146055;
   Best Local Similarity   99.9%;   Pred. No. 0;
   Matches 1784;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db    138575 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC
138634

Qy        61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Db    138635 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC
138694

Qy       121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Db    138695 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG
138754

Qy       181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db    138755 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT
138814

Qy       241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db    138815 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA
138874

Qy       301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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138934

Qy       361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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138994
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Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db     138995 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC
139054

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Db     139055 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC
139114

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Db     139115 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA
139174

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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139234

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Db     139235 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC
139294

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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139354

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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139414

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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139474

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139534

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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139594

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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139834

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139894

Qy         1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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140014

Qy         1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Qy         1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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140314

Qy         1741 GAAGACACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
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RESULT 15
CNS01RGT

LOCUS   CNS01RGT   206256 bp   DNA   linear   PRI 10-JUL-2001
DEFINITION   Human chromosome 14 DNA sequence BAC R-486O13 of library RPCI-11
                from chromosome 14 of Homo sapiens (Human), complete sequence.
ACCESSION   AL160191
VERSION   AL160191.3 GI:14715172
KEYWORDS   HTG; HTGS_ACTIVEFIN.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 206256)
  AUTHORS   Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,
                Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F.,
                Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C.,
                Gyapay,G., Saurin,W. and Weissenbach,J.
  TITLE   Sequencing of the human chromosome 14
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 206256)
  AUTHORS   Genoscope.
  TITLE   Direct Submission
  JOURNAL   Submitted (09-JUL-2001) Genoscope - Centre National de Sequencage :
                BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                - Web : www.genoscope.cns.fr)
COMMENT   On Jul 12, 2001 this sequence version replaced gi:7708226.
                --------------- Genome Center
                Center: Genoscope / Centre National de Sequencage
                Center code: GS
                Web site: http://www.genoscope.cns.fr/
                Contact: SeqRef@genoscope.cns.fr

                The following BAC sequence is oriented from the T7 to the SP6 end.
                Upstream BAC (overlapping the T7 end) : R-718G2 (AC=AL356804)
                Downstream BAC (overlapping the SP6 end) : R-1023I22
                --------------- Summary Statistics
                Assembly program: Phrap; version 2.0
                Quality coverage: 8.36x in Q20 bases; sum-of-contigs
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                Overall quality chart :
                Range   :   bases
                0   :
                1 - 9 :   7
                10 - 19 :   78
                20 - 29 :   197
                30 - 39 :   1106
                40 - 49 :   5627
                50 - 59 :   11755
                60 - 69 :   10922
                70 - 79 :   18529
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                Percentage of bases with a quality value >= 40 : 99 %.
FEATURES   Location/Qualifiers

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                RHdb:RH103433
                dbSTS:STS70962
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STS             72147. .72239
                /note="matching EMBL:G37613
                RHdb:RH101557
                RHdb:RH82090
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STS             118337. .118551
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                RHdb:RH44806
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STS             145994. .146150
                /note="matching EMBL:T17195
                RHdb:RH78238
                dbSTS:STS54980
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                /note="matching EMBL:H15034
                RHdb:RH53547
                dbSTS:STS14940
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                /note="matching EMBL:Z23692
                RHdb:RH9565
                dbSTS:STS25409
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                /note="matching EMBL:Z23692
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ORIGIN
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Query Match              95.7%;   Score 1782.8;   DB 9;   Length 206256;
Best Local Similarity    99.9%;   Pred. No. 0;
Matches 1784;   Conservative    0;   Mismatches    2;   Indels    0;   Gaps    0;

Qy        1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Qy      121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Qy      241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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Qy         1741  GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
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Search completed: June 25, 2004, 12:31:18
Job time : 7017.69 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2004, 00:42:04 ; Search time 653.599 Seconds
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Title: US-10-054-680-3
Perfect score: 1863
Sequence: 1 atggcgtggttaaggttgca..........ggaaagccagtattgggtga 1863

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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        Pred. No. is the number of results predicted by chance to have a
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                              SUMMARIES
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Result   Query
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     7 1784.4   95.8   2534   7   ACC00414   Acc00414 Human 690

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    16    785.2    42.1    1836   4   AAI19464              Aai19464 Probe #93
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    20    785.2    42.1    1836   4   AAK12937              Aak12937 Human bra
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    27    692.4    37.2    4291   3   AAC75706              Aac75706 Human ORF
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    29      319    17.1   24221   4   ABL09808              Abl09808 Drosophil
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    31    164.2     8.8     459   4   ABA51807              Aba51807 Human foe
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    33    164.2     8.8     459   4   ABA21636              Aba21636 Probe #10
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ALIGNMENTS

RESULT 1
ABQ78862
ID   ABQ78862 standard; cDNA; 1863 BP.
XX
AC   ABQ78862;
XX
DT   09-OCT-2002   (first entry)
XX
DE   Human ion exchanger protein #2 cDNA.
XX
KW   Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
KW   antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
KW   gene; ss; chromosome 14.
XX

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OS    Homo sapiens.
XX
FH    Key                 Location/Qualifiers
FT    CDS                 1. .1863
FT                        /*tag=  a
FT                        /product= "Ion exchanger protein 2"
XX
PN    WO200259316-A2.
XX
PD    01-AUG-2002.
XX
PF    22-JAN-2002; 2002WO-US001817.
XX
PR    23-JAN-2001; 2001US-0263384P.
XX
PA    (LEXI-) LEXICON GENETICS INC.
XX
PI    Friddle CJ,  Hilbun E;
XX
DR    WPI; 2002-599791/64.
DR    P-PSDB; ABB81914.
XX
PT    Novel polynucleotides encoding human ion exchanger proteins that are
PT    structurally related to mammalian sodium-calcium exchanger proteins,
PT    useful for drug screening, diagnosis and in gene therapy of biological
PT    disorders.
XX
PS    Disclosure; Page 39-40; 42pp; English.
XX
CC    The invention relates to a novel human ion exchanger protein (NHIEP),
CC    that shares structural similarity with mammalian sodium-calcium exchanger
CC    proteins, and potassium dependent versions of the same. The NHIEP of the
CC    invention has nootropic, cytostatic, antiarthritic, and virucide
CC    activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC    be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC    or to therapeutically augment the efficacy of chemotherapeutic agents
CC    used in the treatment of cancer, arthritis, or as antiviral agents. The
CC    sequence encodes a NHIEP of the invention
XX
SQ    Sequence 1863 BP; 464 A; 426 C; 514 G; 459 T; 0 U; 0 Other;

   Query Match              100.0%;  Score 1863;  DB 6;  Length 1863;
   Best Local Similarity    100.0%;  Pred. No. 0;
   Matches 1863;  Conservative   0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Qy      121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Qy    181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db    361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

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Qy    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Qy    781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Qy    841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Qy    1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200

Qy    1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260

Qy    1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320

Qy    1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

Qy    1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440

Qy    1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

Qy    1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560

Qy    1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620

Qy    1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680

Qy    1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy    1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800

Qy    1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGG 1860
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGG 1860

Qy    1861 TGA 1863
           |||
```

RESULT 2
ABQ78861
ID   ABQ78861 standard; cDNA; 2766 BP.
XX
AC   ABQ78861;
XX
DT   09-OCT-2002   (first entry)
XX
DE   Human ion exchanger protein #1 cDNA.
XX
KW   Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
KW   antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
KW   gene; ss; chromosome 14.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1. .2766
FT   /*tag= a
FT   /product= "Ion exchanger protein 1"
XX
PN   WO200259316-A2.
XX
PD   01-AUG-2002.
XX
PF   22-JAN-2002; 2002WO-US001817.
XX
PR   23-JAN-2001; 2001US-0263384P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Friddle CJ, Hilbun E;
XX
DR   WPI; 2002-599791/64.
DR   P-PSDB; ABB81913.
XX
PT   Novel polynucleotides encoding human ion exchanger proteins that are
PT   structurally related to mammalian sodium-calcium exchanger proteins,
PT   useful for drug screening, diagnosis and in gene therapy of biological
PT   disorders.
XX
PS   Claim 1; Page 36-37; 42pp; English.
XX
CC   The invention relates to a novel human ion exchanger protein (NHIEP),
CC   that shares structural similarity with mammalian sodium-calcium exchanger
CC   proteins, and potassium dependent versions of the same. The NHIEP of the
CC   invention has nootropic, cytostatic, antiarthritic, and virucide
CC   activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC   be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC   or to therapeutically augment the efficacy of chemotherapeutic agents
CC   used in the treatment of cancer, arthritis, or as antiviral agents. The
CC   sequence encodes a NHIEP of the invention
XX
SQ   Sequence 2766 BP; 655 A; 678 C; 760 G; 673 T; 0 U; 0 Other;

```
Query Match        95.8%;  Score 1784.6;  DB 6;  Length 2766;
Best Local Similarity   98.5%;  Pred. No. 0;
Matches 1813;  Conservative   0;  Mismatches   24;  Indels    4;  Gaps    1;

Qy        1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy       61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy      121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy      181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy      241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300

Qy      301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy      361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy      421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy      481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540

Qy      541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

Qy      601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660

Qy      661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

Qy      721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
```

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Qy    781  ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC  840

Qy    841  CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC  900

Qy    901  CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC  960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC  960

Qy    961  AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT  1020

Qy   1021  TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT  1080

Qy   1081  ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC  1140

Qy   1141  TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT  1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT  1200

Qy   1201  GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG  1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG  1260

Qy   1261  AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC  1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC  1320

Qy   1321  AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC  1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC  1380

Qy   1381  CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC  1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC  1440

Qy   1441  TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA  1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441  TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA  1500

Qy   1501  GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA  1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA  1560

Qy   1561  GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT  1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT  1620

Qy   1621  GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT  1680
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621  GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680

Qy    1681  ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681  ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy    1741  GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
              ||||||||||||||||||||||||||||||||||||||||||||     |||||  |   ||   |
Db    1741  GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1796

Qy    1801  GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
              | | |   || |  ||| |||||||    |     |   |||||
Db    1797  GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837
```

RESULT 3
ABQ78864
```
ID    ABQ78864 standard; cDNA; 2766 BP.
XX
AC    ABQ78864;
XX
DT    09-OCT-2002  (first entry)
XX
DE    Human ion exchanger protein #1 cDNA A/G mutant.
XX
KW    Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
KW    antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
KW    gene; ss; mutant.
XX
OS    Homo sapiens.
OS    Synthetic.
XX
FH    Key              Location/Qualifiers
FT    mutation         replace(1889,A)
FT                     /*tag=  a
XX
PN    WO200259316-A2.
XX
PD    01-AUG-2002.
XX
PF    22-JAN-2002; 2002WO-US001817.
XX
PR    23-JAN-2001; 2001US-0263384P.
XX
PA    (LEXI-) LEXICON GENETICS INC.
XX
PI    Friddle CJ,  Hilbun E;
XX
DR    WPI; 2002-599791/64.
XX
PT    Novel polynucleotides encoding human ion exchanger proteins that are
PT    structurally related to mammalian sodium-calcium exchanger proteins,
PT    useful for drug screening, diagnosis and in gene therapy of biological
PT    disorders.
XX
PS    Disclosure; Page; 42pp; English.
```

    Query Match   95.8%;   Score 1784.6;   DB 6;   Length 2766;
    Best Local Similarity   98.5%;   Pred. No. 0;
    Matches 1813;   Conservative   0;   Mismatches   24;   Indels   4;   Gaps   1;

Qy   1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy   61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              |||||||||||||||||||||,||||||||||||||||||||||||||||||||||||||||
Db   61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy   121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy   181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy   241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300

Qy   301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy   361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy   421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy   481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540

Qy   541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db    541  ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA  600

Qy    601  CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT  660

Qy    661  CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC  720

Qy    721  TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC  780

Qy    781  ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC  840

Qy    841  CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC  900

Qy    901  CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC  960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC  960

Qy    961  AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020

Qy   1021  TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080

Qy   1081  ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140

Qy   1141  TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200

Qy   1201  GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGCTGTACTCCTGACAGTGGTGAGG 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGCTGTACTCCTGACAGTGGTGAGG 1260

Qy   1261  AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320

Qy   1321  AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

Qy   1381  CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Qy    1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

Qy    1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560

Qy    1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620

Qy    1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680

Qy    1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy    1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
           ||||||||||||||||||||||||||||||||||||||||    ||||| |  || |
Db    1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1796

Qy    1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
           |  |  || | ||| |||||||  |    |     |||||
Db    1797 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837


RESULT 4
ABQ78866
ID    ABQ78866 standard; cDNA; 2769 BP.
XX
AC    ABQ78866;
XX
DT    09-OCT-2002  (first entry)
XX
DE    Human ion exchanger protein #1 cDNA A/G+GCA mutant.
XX
KW    Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
KW    antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
KW    gene; ss; mutant.
XX
OS    Homo sapiens.
OS    Synthetic.
XX
FH    Key             Location/Qualifiers
FT    mutation        replace(1889,A)
FT                    /*tag=   a
FT    mutation        replace(2113. .2115,-)
FT                    /*tag=   b
XX
PN    WO200259316-A2.
XX
PD    01-AUG-2002.
XX
```

PT   Novel polynucleotides encoding human ion exchanger proteins that are
PT   structurally related to mammalian sodium-calcium exchanger proteins,
PT   useful for drug screening, diagnosis and in gene therapy of biological
PT   disorders.
XX
PS   Disclosure; Page; 42pp; English.
XX
CC   The invention relates to a novel human ion exchanger protein (NHIEP),
CC   that shares structural similarity with mammalian sodium-calcium exchanger
CC   proteins, and potassium dependent versions of the same. The NHIEP of the
CC   invention has nootropic, cytostatic, antiarthritic, and virucide
CC   activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC   be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC   or to therapeutically augment the efficacy of chemotherapeutic agents
CC   used in the treatment of cancer, arthritis, or as antiviral agents. The
CC   sequence represents a mutant form of a NHIEP of the invention. Note: The
CC   present sequence is not shown in the specification but is derived from
CC   the human NHIEP sequence shown as SEQ ID 1 (ABQ78861)
XX
SQ   Sequence 2769 BP; 655 A; 679 C; 762 G; 673 T; 0 U; 0 Other;

     Query Match   95.8%;   Score 1784.6;   DB 6;   Length 2769;
     Best Local Similarity   98.5%;   Pred. No. 0;
     Matches 1813; Conservative   0; Mismatches   24; Indels   4; Gaps   1;

Qy   1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy   61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy   121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy   181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy   241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300

Qy   301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db      301  TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA  360

Qy      361  ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361  ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC  420

Qy      421  CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421  CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC  480

Qy      481  ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC  540
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||│
Db      481  ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC  540

Qy      541  ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541  ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA  600

Qy      601  CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601  CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT  660

Qy      661  CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661  CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC  720

Qy      721  TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721  TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC  780

Qy      781  ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC  840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781  ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC  840

Qy      841  CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC  900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841  CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC  900

Qy      901  CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901  CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC  960

Qy      961  AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961  AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT  1020

Qy     1021  TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021  TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT  1080

Qy     1081  ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC  1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081  ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC  1140

Qy     1141  TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141  TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT  1200
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Qy     1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260

Qy     1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320

Qy     1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

Qy     1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440

Qy     1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

Qy     1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560

Qy     1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620

Qy     1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680

Qy     1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy     1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
            |||||||||||||||||||||||||||||||||||||||||||||     ||||| |  || |
Db     1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1796

Qy     1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
            | | |  || | ||| |||||||  |     |      |||||
Db     1797 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837


RESULT 5
ABQ78865
ID   ABQ78865 standard; cDNA; 2769 BP.
XX
AC   ABQ78865;
XX
DT   09-OCT-2002  (first entry)
XX
DE   Human ion exchanger protein #1 cDNA GCA mutant.
XX
KW   Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
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KW    antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
KW    gene; ss; mutant.
XX
OS    Homo sapiens.
OS    Synthetic.
XX
FH    Key             Location/Qualifiers
FT    mutation        replace(2113. .2115,-)
FT                    /*tag=  a
XX
PN    WO200259316-A2.
XX
PD    01-AUG-2002.
XX
PF    22-JAN-2002; 2002WO-US001817.
XX
PR    23-JAN-2001; 2001US-0263384P.
XX
PA    (LEXI-) LEXICON GENETICS INC.
XX
PI    Friddle CJ,  Hilbun E;
XX
DR    WPI; 2002-599791/64.
XX
PT    Novel polynucleotides encoding human ion exchanger proteins that are
PT    structurally related to mammalian sodium-calcium exchanger proteins,
PT    useful for drug screening, diagnosis and in gene therapy of biological
PT    disorders.
XX
PS    Disclosure; Page; 42pp; English.
XX
CC    The invention relates to a novel human ion exchanger protein (NHIEP),
CC    that shares structural similarity with mammalian sodium-calcium exchanger
CC    proteins, and potassium dependent versions of the same. The NHIEP of the
CC    invention has nootropic, cytostatic, antiarthritic, and virucide
CC    activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC    be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC    or to therapeutically augment the efficacy of chemotherapeutic agents
CC    used in the treatment of cancer, arthritis, or as antiviral agents. The
CC    sequence represents a mutant form of a NHIEP of the invention. Note: The
CC    present sequence is not shown in the specification but is derived from
CC    the human NHIEP sequence shown as SEQ ID 1 (ABQ78861)
XX
SQ    Sequence 2769 BP; 656 A; 679 C; 761 G; 673 T; 0 U; 0 Other;
```

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   Query Match              95.8%;  Score 1784.6;  DB 6;  Length 2769;
   Best Local Similarity  98.5%;  Pred. No. 0;
   Matches 1813; Conservative    0; Mismatches   24; Indels   4; Gaps    1;

Qy        1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy       61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Qy    121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy    181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy    241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300

Qy    301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy    361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy    421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540

Qy    541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

Qy    601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660

Qy    661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

Qy    721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780

Qy    781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840

Qy    841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900

Qy    901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960

Qy    961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961  AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020

Qy     1021  TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021  TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080

Qy     1081  ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081  ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140

Qy     1141  TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141  TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200

Qy     1201  GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201  GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260

Qy     1261  AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261  AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320

Qy     1321  AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321  AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

Qy     1381  CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381  CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440

Qy     1441  TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1441  TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

Qy     1501  GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1501  GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560

Qy     1561  GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1561  GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620

Qy     1621  GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1621  GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680

Qy     1681  ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1681  ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy     1741  GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
             |||||||||||||||||||||||||||||||||||||||||      |||||  |   ||    |
Db     1741  GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1796

Qy     1801  GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
             |  |   || |  |||  |||||||     |     |     |||||
```

RESULT 6
ABQ78863
ID   ABQ78863 standard; cDNA; 3812 BP.
XX
AC   ABQ78863;
XX
DT   09-OCT-2002   (first entry)
XX
DE   Human ion exchanger protein cDNA #3.
XX
KW   Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
KW   antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
KW   gene; ss; chromosome 14.
XX
OS   Homo sapiens.
XX
PN   WO200259316-A2.
XX
PD   01-AUG-2002.
XX
PF   22-JAN-2002; 2002WO-US001817.
XX
PR   23-JAN-2001; 2001US-0263384P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Friddle CJ, Hilbun E;
XX
DR   WPI; 2002-599791/64.
XX
PT   Novel polynucleotides encoding human ion exchanger proteins that are
PT   structurally related to mammalian sodium-calcium exchanger proteins,
PT   useful for drug screening, diagnosis and in gene therapy of biological
PT   disorders.
XX
PS   Disclosure; Page 41-42; 42pp; English.
XX
CC   The invention relates to a novel human ion exchanger protein (NHIEP),
CC   that shares structural similarity with mammalian sodium-calcium exchanger
CC   proteins, and potassium dependent versions of the same. The NHIEP of the
CC   invention has nootropic, cytostatic, antiarthritic, and virucide
CC   activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC   be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC   or to therapeutically augment the efficacy of chemotherapeutic agents
CC   used in the treatment of cancer, arthritis, or as antiviral agents. The
CC   sequence encodes a NHIEP of the invention, with regions of flanking
CC   sequence
XX
SQ   Sequence 3812 BP; 860 A; 1059 C; 1041 G; 852 T; 0 U; 0 Other;

    Query Match   95.8%; Score 1784.6; DB 6; Length 3812;
    Best Local Similarity 98.5%; Pred. No. 0;
    Matches 1813; Conservative   0; Mismatches   24; Indels   4; Gaps   1;

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Qy       1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     618 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 677

Qy      61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     678 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 737

Qy     121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     738 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 797

Qy     181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     798 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 857

Qy     241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     858 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 917

Qy     301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     918 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 977

Qy     361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     978 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 1037

Qy     421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1038 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 1097

Qy     481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1098 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 1157

Qy     541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1158 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 1217

Qy     601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1218 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1277

Qy     661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1278 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1337

Qy     721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1338 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1397

Qy     781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1398 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 1457

Qy     841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1458  CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC  1517

Qy       901  CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC  960
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1518  CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC  1577

Qy       961  AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT  1020
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1578  AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT  1637

Qy      1021  TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT  1080
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1638  TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT  1697

Qy      1081  ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC  1140
                   |||||||||||||||||||||||||||||||||||'|||||||||||||||||||||||
Db      1698  ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC  1757

Qy      1141  TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT  1200
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1758  TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT  1817

Qy      1201  GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG  1260
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1818  GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG  1877

Qy      1261  AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC  1320
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1878  AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC  1937

Qy      1321  AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC  1380
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1938  AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC  1997

Qy      1381  CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC  1440
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1998  CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC  2057

Qy      1441  TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA  1500
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2058  TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA  2117

Qy      1501  GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA  1560
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2118  GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA  2177

Qy      1561  GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT  1620
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2178  GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT  2237

Qy      1621  GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT  1680
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2238  GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT  2297

Qy      1681  ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT  1740
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      2298 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2357

Qy      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
             ||||||||||||||||||||||||||||||||||||||||||||||    ||||| | || |
Db      2358 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 2413

Qy      1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
             | | | || | ||| |||||||   |    |    |||||
Db      2414 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 2454
```

RESULT 7
ACC00414
ID   ACC00414 standard; cDNA; 2534 BP.
XX
AC   ACC00414;
XX
DT   04-JUL-2003   (first entry)
XX
DE   Human 69039 coding sequence.
XX
KW   Human; 69039; neuroprotective; gene therapy; haematopoietic disorder;
KW   Na+/Ca2+ exchanger; ion transporter; neural tissue;
KW   neurological disorder; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   343. .2130
FT   /*tag= a
FT   /product= "Human 69039"
XX
PN   WO2003029410-A2.
XX
PD   10-APR-2003.
XX
PF   27-SEP-2002; 2002WO-US030817.
XX
PR   28-SEP-2001; 2001US-0325737P.
XX
PA   (MILL-) MILLENIUM PHARM INC.
XX
PI   Carroll JM;
XX
DR   WPI; 2003-381617/36.
DR   P-PSDB; ABR40134.
XX
PT   Identifying a nucleic acid molecule associated with a disorder for
PT   preparing a composition for treating hematopoietic or neurological
PT   disorder by detecting the presence of a nucleic acid molecule in the
PT   sample that is amplified.
XX
PS   Claim 1; Page 109-110; 133pp; English.
XX
CC   The present sequence is the coding sequence for human 69039, a novel
CC   Na+/Ca2+ exchanger family member (ion transporter). 69039 was shown to be
CC   expressed in human haematopoietic cells, e.g. CD34-expressing progenitor
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CC    cells as well as in neural tissues, e.g. brain cortex and hypothalamus.
CC    69039 may therefore be used for preparing a composition for treating
CC    haematopoietic or neurological disorder
XX
SQ    Sequence 2534 BP; 602 A; 595 C; 644 G; 693 T; 0 U; 0 Other;

      Query Match                95.8%;   Score 1784.4;   DB 7;   Length 2534;
      Best Local Similarity      99.9%;   Pred. No. 0;
      Matches 1785;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

Qy        1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      343 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 402

Qy       61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      403 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 462

Qy      121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      463 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 522

Qy      181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      523 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 582

Qy      241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      583 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 642

Qy      301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      643 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 702

Qy      361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      703 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 762

Qy      421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      763 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 822

Qy      481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      823 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 882

Qy      541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      883 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 942

Qy      601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      943 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1002

Qy      661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1003 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1062

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Qy    721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1063 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1122

Qy    781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1123 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 1182

Qy    841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1183 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 1242

Qy    901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1243 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1302

Qy    961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1303 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1362

Qy   1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1363 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1422

Qy   1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1423 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1482

Qy   1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1483 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1542

Qy   1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1543 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1602

Qy   1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1603 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1662

Qy   1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1663 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1722

Qy   1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1723 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1782

Qy   1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1783 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1842

Qy   1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1843 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1902
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Qy    1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
           |||||||||||||||||||||||||||I|||||||||||||||||||||||||||||||||
Db    1903 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1962

Qy    1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1963 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 2022

Qy    1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2023 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2082

Qy    1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
           |||||||||||||||||||||||||||||||||||||||||||| |
Db    2083 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGT 2128


RESULT 8
ABA04756
ID   ABA04756 standard; cDNA; 2781 BP.
XX
AC   ABA04756;
XX
DT   25-FEB-2002   (first entry)
XX
DE   Human natrium(+)-calcium(2+) exchanger form 3 protein, HNCX3, cDNA.
XX
KW   Human; Natrium(+)-Calcium(2+) exchanger form 3; HNCX3; chromosome 14;
KW   cardiac failure; myocardial infarction; cardiac hypertrophy; arrhythmia;
KW   myocarditis; pulmonary hypertension; cardiotoxicity; cardiant; Vaccine;
KW   coronary heart disease; renal failure; ischaemic disorder;
KW   Antiarrhythmic; Vasotropic; Hypotensive; cardiovascular disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key              Location/Qualifiers
FT   CDS              1. .2781
FT                    /*tag=  a
FT                    /partial
FT                    /product= "Human natrium(+)-calcium(2+) exchanger form 3
FT                    protein, HNCX3"
FT                    /note= "No stop codon given"
XX
PN   WO200183744-A2.
XX
PD   08-NOV-2001.
XX
PF   30-APR-2001; 2001WO-EP004886.
XX
PR   02-MAY-2000; 2000EP-00109080.
XX
PA   (MERE ) MERCK PATENT GMBH.
XX
PI   Wilm C;
XX
DR   WPI; 2002-041493/05.
DR   P-PSDB; AAM47745.
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    Query Match   95.7%;   Score 1783;   DB 6;   Length 2781;
    Best Local Similarity 98.4%;   Pred. No. 0;
    Matches 1812; Conservative   0; Mismatches   25; Indels   4; Gaps   1;

Qy   1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy   61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy   121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy   181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy   241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300

Qy   301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy   361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy   421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy   481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540

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Qy          541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

Qy          601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660

Qy          661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

Qy          721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780

Qy          781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840

Qy          841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900

Qy          901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960

Qy          961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020

Qy         1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
                |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db         1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGTGCCTTCTACCGTATCCAAGCCACTCGT 1080

Qy         1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140

Qy         1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Qy         1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260

Qy         1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320

Qy         1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Qy    1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||.|||||||
Db    1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440

Qy    1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Db    1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

Qy    1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Db    1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560

Qy    1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620

Qy    1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680

Qy    1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy    1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
           ||||||||||||||||||||||||||||||||||||||||     ||||| |   || |
Db    1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1796

Qy    1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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Db    1797 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837
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RESULT 9
ABN83428

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ID   ABN83428 standard; cDNA; 2782 BP.
XX
AC   ABN83428;
XX
DT   21-AUG-2002  (first entry)
XX
DE   Human transporter protein coding sequence.
XX
KW   Human; sodium/calcium exchanger; transporter; brain; heart; kidney; lung;
KW   spleen; testis; leukocyte; foetal brain; chromosome 14; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             10. .2775
FT                   /*tag=  a
FT                   /product= "Human transporter"
XX
PN   WO200233086-A2.
XX
PD   25-APR-2002.
XX
```

PT   Human transporter peptide related to sodium/calcium exchanger subfamily
PT   for identifying modulators useful for treating a disease or condition
PT   mediated by human transporter protein.
XX
PS   Claim 4; Fig 1; 200pp; English.
XX
CC   The present sequence is the coding sequence of a human transporter
CC   protein, which is related to the sodium/calcium exchanger subfamily.
CC   Experimental data indicates expression of the transporter gene in humans
CC   in brain, heart, kidney, lung, spleen, testis, leukocyte and foetal
CC   brain. The gene of the transporter was mapped to chromosome 14 by ePCR
XX
SQ   Sequence 2782 BP; 655 A; 685 C; 766 G; 676 T; 0 U; 0 Other;

   Query Match   95.7%; Score 1783; DB 6; Length 2782;
   Best Local Similarity   98.4%; Pred. No. 0;
   Matches 1812; Conservative   0; Mismatches   25; Indels   4; Gaps   1;

Qy   1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   10 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 69

Qy   61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   70 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 129

Qy   121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   130 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 189

Qy   181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   190 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 249

Qy   241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   250 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 309

Qy   301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   310 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 369

Qy   361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db    370  ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC  429

Qy    421  CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    430  CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC  489

Qy    481  ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    490  ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC  549

Qy    541  ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    550  ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA  609

Qy    601  CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    610  CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT  669

Qy    661  CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    670  CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC  729

Qy    721  TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    730  TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC  789

Qy    781  ATGCACAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    790  ATGCACAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC  849

Qy    841  CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    850  CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC  909

Qy    901  CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC  960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    910  CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATCCTC  969

Qy    961  AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    970  AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT  1029

Qy    1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1030 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT  1089

Qy    1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1090 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC  1149

Qy    1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT  1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1150 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT  1209

Qy    1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG  1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1210 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG  1269
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Qy    1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1270 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1329

Qy    1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1330 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1389

Qy    1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1390 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1449

Qy    1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1450 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1509

Qy    1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1510 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1569

Qy    1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1570 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1629

Qy    1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1630 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1689

Qy    1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1690 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1749

Qy    1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
           |||||||||||||||||||||||||||||||||||||||||     |||||  |  ||  |
Db    1750 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1805

Qy    1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
           |  |  || | ||| |||||||   |   |   |||||
Db    1806 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1846


RESULT 10
ABZ33735
ID    ABZ33735 standard; cDNA; 2966 BP.
XX
AC    ABZ33735;
XX
DT    30-JAN-2003  (first entry)
XX
DE    Human TRICH encoding cDNA SEQ ID NO 41.
XX
KW    Human; TRICH; transporter and ion channel; transport disorder;
KW    cystic fibrosis; diabetes mellitus; Parkinson's disease; cancer;
KW    neurological disorder; Alzheimer's disease; Huntington's disease;
KW    immunological disorder; AIDS; asthma; cell proliferative disorder;
KW    transgenic; gene therapy; neuroprotective; antidiabetic; cytostatic;
```

PT   Novel human transporter and ion channel polypeptide, useful in diagnosis,
PT   prevention or treatment of transport, neurological, muscle, immunological
PT   and cell proliferative disorders.
XX
PS   Claim 96; SEQ ID NO 41; 146pp + Sequence Listing; English.
XX
CC   The invention relates to human transporter and ion channel polypeptide
CC   (TRICH) (I) selected from one of 32 polypeptide sequences (ABP74096-
CC   ABP74127), a naturally occurring polypeptide comprising a sequence having
CC   at least sequence 90 % identity to (I) or a biologically active or
CC   immunogenic fragment of (I). (I) is useful for screening a compound for
CC   effectiveness as an agonist or antagonist, for screening a compound that
CC   specifically binds (I) or modulates the activity of (I) and for preparing
CC   a polyclonal or monoclonal antibody by hybridoma technology.
CC   Polynucleotides (II, ABZ33727-ABZ33758) encoding (I) are useful for
CC   screening a compound altering gene expression. (I) and (II) are useful in
CC   a diagnostic tests for a condition or a disease associated with the
CC   expression of TRICH in a biological sample, especially disorders selected
CC   from a transport disorder such as cystic fibrosis, diabetes mellitus,
CC   Parkinson's disease, cardiac disorders, neurological disorders such as
CC   Alzheimer's disease, Huntington's disease, muscle disorders,
CC   immunological disorder such as AIDS, asthma and atherosclerosis, and cell
CC   proliferative disorder such as arteriosclerosis, cirrhosis, hepatitis and
CC   cancer. (II) is useful for creating knock-in humanised animals or
CC   transgenic animals to model human diseases, in somatic or germline gene

SQ   Sequence 2966 BP; 692 A; 725 C; 809 G; 740 T; 0 U; 0 Other;

    Query Match   95.7%; Score 1783; DB 6;   Length 2966;
    Best Local Similarity   98.4%; Pred. No. 0;
    Matches 1812; Conservative   0; Mismatches   25; Indels   4; Gaps   1;

Qy   1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   201 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 260

Qy   61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   261 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 320

Qy   121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   321 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 380

Qy   181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Qy   241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Qy   301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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RESULT 11
ABN83429
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XX
AC    ABN83429;
XX
DT    21-AUG-2002   (first entry)
XX
DE    Human transporter protein gene.
XX
KW    Human; sodium/calcium exchanger; transporter; brain; heart; kidney; lung;
KW    spleen; testis; leukocyte; foetal brain; chromosome 14; gene;
KW    single nucleotide polymorphism; SNP; ds.
XX
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XX
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1784; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

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Qy    1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3570 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 3629

Qy    1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3630 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 3689
```

```
Qy     1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3690 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 3749

Qy     1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
            ||||||||||||||||||||||||||||||||||||||||||||| |
Db     3750 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGT 3795
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RESULT 12
ABX56261
ID   ABX56261 standard; DNA; 2813 BP.
XX
AC   ABX56261;
XX
DT   19-FEB-2003   (first entry)
XX
DE   Human NOV1a CG56258-01 DNA SEQ ID 1.
XX
KW   NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
KW   metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
KW   antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
KW   cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
KW   anorexia; neurodegenerative disorder; Alzheimer's disease; cancer; gene;
KW   Parkinson's disease; haematopoietic disorder; metabolic disturbance;
KW   metabolic syndrome X; wasting disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200281625-A2.
XX
PD   17-OCT-2002.
XX
PF   03-APR-2002; 2002WO-US010366.
XX
PR   03-APR-2001; 2001US-0281086P.
PR   05-APR-2001; 2001US-0281906P.
PR   06-APR-2001; 2001US-0282020P.
PR   10-APR-2001; 2001US-0282930P.
PR   12-APR-2001; 2001US-0283444P.
PR   12-APR-2001; 2001US-0283512P.
PR   13-APR-2001; 2001US-0283657P.
PR   13-APR-2001; 2001US-0283678P.
PR   13-APR-2001; 2001US-0283710P.
PR   17-APR-2001; 2001US-0284234P.
PR   19-APR-2001; 2001US-0285325P.
PR   20-APR-2001; 2001US-0285381P.
PR   24-APR-2001; 2001US-0286068P.
PR   25-APR-2001; 2001US-0286292P.
PR   07-JUN-2001; 2001US-0296692P.
PR   26-JUN-2001; 2001US-0300883P.
PR   08-AUG-2001; 2001US-0311003P.
PR   13-AUG-2001; 2001US-0311973P.
PR   16-AUG-2001; 2001US-0312901P.
PR   14-SEP-2001; 2001US-0322283P.
PR   05-OCT-2001; 2001US-0327448P.
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Db     69 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 128

Qy    121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    129 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 188

Qy    181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    189 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 248

Qy    241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    249 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 308

Qy    301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    309 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 368

Qy    361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||!|||||||
Db    369 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 428

Qy    421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    429 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 488

Qy    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    489 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 548

Qy    541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    549 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 608

Qy    601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    609 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 668

Qy    661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    669 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 728

Qy    721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    729 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 788

Qy    781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    789 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 848

Qy    841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    849 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 908

Qy    901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    909 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 968
```

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Qy    961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    969 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1028

Qy   1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
          ||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   1029 TACTATGCTCTTTCCCACCAACAGAAGAGCCGTGCCTTCTACCGTATCCAAGCCACTCGT 1088

Qy   1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1089 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1148

Qy   1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1149 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1208

Qy   1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1209 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1268

Qy   1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1269 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1328

Qy   1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1329 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1388

Qy   1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1389 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1448

Qy   1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1449 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1508

Qy   1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1509 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1568

Qy   1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1569 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1628

Qy   1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1629 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1688

Qy   1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1689 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1748

Qy   1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGT 1784
          ||||||||||||||||||||||||||||||||||||||||||||
Db   1749 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGT 1792
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RESULT 13
ABX56262
ID   ABX56262 standard; DNA; 2840 BP.
XX
AC   ABX56262;
XX
DT   19-FEB-2003 (first entry)
XX
DE   Human NOV1b CG56558-02 DNA SEQ ID 3.
XX
KW   NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
KW   metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
KW   antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
KW   cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
KW   anorexia; neurodegenerative disorder; Alzheimer's disease; cancer; gene;
KW   Parkinson's disease; haematopoietic disorder; metabolic disturbance;
KW   metabolic syndrome X; wasting disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200281625-A2.
XX
PD   17-OCT-2002.
XX
PF   03-APR-2002; 2002WO-US010366.
XX
PR   03-APR-2001; 2001US-0281086P.
PR   05-APR-2001; 2001US-0281906P.
PR   06-APR-2001; 2001US-0282020P.
PR   10-APR-2001; 2001US-0282930P.
PR   12-APR-2001; 2001US-0283444P.
PR   12-APR-2001; 2001US-0283512P.
PR   13-APR-2001; 2001US-0283657P.
PR   13-APR-2001; 2001US-0283678P.
PR   13-APR-2001; 2001US-0283710P.
PR   17-APR-2001; 2001US-0284234P.
PR   19-APR-2001; 2001US-0285325P.
PR   20-APR-2001; 2001US-0285381P.
PR   24-APR-2001; 2001US-0286068P.
PR   25-APR-2001; 2001US-0286292P.
PR   07-JUN-2001; 2001US-0296692P.
PR   26-JUN-2001; 2001US-0300883P.
PR   08-AUG-2001; 2001US-0311003P.
PR   13-AUG-2001; 2001US-0311973P.
PR   16-AUG-2001; 2001US-0312901P.
PR   14-SEP-2001; 2001US-0322283P.
PR   05-OCT-2001; 2001US-0327448P.
PR   31-DEC-2001; 2001US-0345734P.
PR   03-JAN-2002; 2002US-0345755P.
PR   04-FEB-2002; 2002US-0354391P.
PR   02-APR-2002; 2002US-00114153.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Padigaru M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD;
PI   Smithson G, Guo X, Gerlach V, Casman SJ, Boldog FL, Li L;

PI Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM, Spytek KA;
PI Malyankar UM, Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J;
PI Peyman JA, Catterton E, Macdougall JR, Edinger SR, Stone DJ;
PI Mazur A;
XX
PT New isolated NOVX polypeptide useful for treating cardiomyopathy,
PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious
PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
PT cancer.
XX
PS Claim 3; Page 84; 425pp; English.
XX
CC This invention describes novel polypeptides, termed NOVX which have
CC antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial,
CC neuroprotective, antiparkinsonian, antilipaemic, cytostatic, nootropic,
CC cardiant and immunomodulatory activity. The polypeptide and any
CC antibodies generated from it are useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease
CC selected from a pathology associated with the NOVX polypeptide. Fragments
CC and portions of the polynucleotides encoding NOVX polypeptides are useful
CC to map the location of NOVX genes on a chromosome, to identify
CC individuals from minute biological samples, as DNA markers for
CC restriction fragment length polymorphism (RFLP), and are useful to
CC prepare polymerase chain reaction primers. The products of the invention
CC can be used in gene therapy and for treating cardiomyopathy, metabolic
CC disorders, diabetes, atherosclerosis, obesity, infectious disease,
CC anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's
CC disease, immune disorders, haematopoietic disorders, and various
CC dyslipidaemias, metabolic disturbances associated with obesity, metabolic
CC syndrome X and wasting disorders associated with chronic diseases and
CC various cancers. ABX56261-ABX56306 represent the polynucleotide fragments
CC which encode the NOVX polypeptides represented in ABU12041-ABU12086
XX
SQ Sequence 2840 BP; 668 A; 700 C; 775 G; 697 T; 0 U; 0 Other;

```
  Query Match              95.7%;  Score 1782.4;  DB 7;  Length 2840;
  Best Local Similarity    99.9%;  Pred. No. 0;
  Matches 1783;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;


Qy        1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       63 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 122

Qy       61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      123 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 182

Qy      121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      183 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 242

Qy      181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      243 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 302
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Qy      241  TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      303  TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA  362

Qy      301  TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      363  TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA  422

Qy      361  ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      423  ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC  482

Qy      421  CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      483  CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC  542

Qy      481  ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      543  ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC  602

Qy      541  ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      603  ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA  662

Qy      601  CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      663  CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT  722

Qy      661  CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      723  CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC  782

Qy      721  TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      783  TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC  842

Qy      781  ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC  840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      843  ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC  902

Qy      841  CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC  900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      903  CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC  962

Qy      901  CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      963  CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC  1022

Qy      961  AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1023 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT  1082

Qy      1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT  1080
             |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db      1083 TACTATGCTCTTTCCCACCAACAGAAGAGCCGTGCCTTCTACCGTATCCAAGCCACTCGT  1142
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Qy   1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
          ||||||||.|||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1143 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1202

Qy   1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1203 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1262

Qy   1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1263 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1322

Qy   1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1323 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1382

Qy   1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1383 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1442

Qy   1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1443 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1502

Qy   1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1503 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1562

Qy   1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1563 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1622

Qy   1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1623 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1682

Qy   1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1683 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1742

Qy   1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1743 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1802

Qy   1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGT 1784
          ||||||||||||||||||||||||||||||||||||||||||||
Db   1803 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGT 1846
```

RESULT 14
ABX56263
ID   ABX56263 standard; DNA; 2685 BP.
XX
AC   ABX56263;
XX
DT   19-FEB-2003 (first entry)
XX

PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious
PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
PT cancer.
XX
PS Claim 3; Page 85-86; 425pp; English.
XX
CC This invention describes novel polypeptides, termed NOVX which have
CC antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial,
CC neuroprotective, antiparkinsonian, antilipaemic, cytostatic, nootropic,
CC cardiant and immunomodulatory activity. The polypeptide and any
CC antibodies generated from it are useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease
CC selected from a pathology associated with the NOVX polypeptide. Fragments
CC and portions of the polynucleotides encoding NOVX polypeptides are useful
CC to map the location of NOVX genes on a chromosome, to identify
CC individuals from minute biological samples, as DNA markers for
CC restriction fragment length polymorphism (RFLP), and are useful to
CC prepare polymerase chain reaction primers. The products of the invention
CC can be used in gene therapy and for treating cardiomyopathy, metabolic
CC disorders, diabetes, atherosclerosis, obesity, infectious disease,
CC anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's
CC disease, immune disorders, haematopoietic disorders, and various
CC dyslipidaemias, metabolic disturbances associated with obesity, metabolic
CC syndrome X and wasting disorders associated with chronic diseases and
CC various cancers. ABX56261-ABX56306 represent the polynucleotide fragments
CC which encode the NOVX polypeptides represented in ABU12041-ABU12086
XX
SQ Sequence 2685 BP; 645 A; 657 C; 741 G; 642 T; 0 U; 0 Other;

```
    Query Match              91.0%;   Score 1694.8;   DB 7;   Length 2685;
    Best Local Similarity    98.2%;   Pred. No. 0;
    Matches 1725;  Conservative    0;  Mismatches   27;  Indels   4;  Gaps   1;

Qy        86 GAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTT 145
             ||  |  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2 GATCCGAGGCTGGTGGCTCAGGGGACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTT 61

Qy       146 CAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTT 205
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        62 CAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTT 121

Qy       206 CCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCC 265
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       122 CCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCC 181

Qy       266 TTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAG 325
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       182 TTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAG 241

Qy       326 AGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACAACCACTATTCGGGTCT 385
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       242 AGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACAACCACTATTCGGGTCT 301

Qy       386 GGAATGAAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATAC 445
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       302 GGAATGAAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATAC 361
```

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Qy    446 TCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTA 505
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    362 TCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTA 421

Qy    506 CCATTGTAGGGAGTGCAGCCTTCAACATGTTCATCATCATTGGCATCTGTGTCTACGTGA 565
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    422 CCATTGTAGGGAGTGCAGCCTTCAACATGTTCATCATCATTGGCATCTGTGTCTACGTGA 481

Qy    566 TCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTT 625
          ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db    482 TCCCAGACGGAGAGACTCGCAAGATCAAACATCTACGAGTCTTCTTCATCACCGCTGCTT 541

Qy    626 GGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGG 685
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    542 GGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGG 601

Qy    686 TCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCT 745
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    602 TCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCT 661

Qy    746 GGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACA 805
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    662 GGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACA 721

Qy    806 AACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATG 865
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    722 AACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATG 781

Qy    866 GGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGAAG 925
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    782 GGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGAAG 841

Qy    926 TGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCAG 985
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    842 TGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCAG 901

Qy    986 AGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAACAGA 1045
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    902 AGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAACAGA 961

Qy   1046 AGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCC 1105
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    962 AGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCC 1021

Qy   1106 TGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCG 1165
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1022 TGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCG 1081

Qy   1166 ATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGG 1225
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1082 ATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGG 1141

Qy   1226 AGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCA 1285
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1142 AGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCA 1201

Qy   1286 TGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCA 1345
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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1202 TGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCA 1261

Qy   1346 CAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAA 1405
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1262 CAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAA 1321

Qy   1406 TTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCA 1465
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1322 TTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCA 1381

Qy   1466 TAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGC 1525
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1382 TAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGC 1441

Qy   1526 CTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATG 1585
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1442 CTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATG 1501

Qy   1586 CAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGTGTTATGG 1645
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1502 CAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGTGTTATGG 1561

Qy   1646 AGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACAGTCATCGTCCCCTTTAGGACAG 1705
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1562 AGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACAGTCATCGTCCCCTTTAGGACAG 1621

Qy   1706 TAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAAT 1765
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1622 TAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAAT 1681

Qy   1766 TCAAGAATGATGAAACTGTATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCC 1825
          |||||||||||||||||    ||||| |  ||  | | |  || | ||| |||||||
Db   1682 TCAAGAATGATGAAAC----TGTGAAAACCATAAGGGTTAAAATAGTAGATGAGGAGGAA 1737

Qy   1826 AAGAGGATAGCAGAGA 1841
          |    |    |||||
Db   1738 TACGAAAGGCAAGAGA 1753


RESULT 15
AAD24450
ID    AAD24450 standard; cDNA; 4087 BP.
XX
AC    AAD24450;
XX
DT    07-MAY-2002   (first entry)
XX
DE    Bovine NCX-1 cDNA.
XX
KW    Bovine; recombinant protein; larvae expression system; membrane protein;
KW    transport protein; cardiac sodium-calcium exchange protein; Na-K ATPase;
KW    NCX1; cystic fibrosis transmembrane conductance regulator; CFTR; vaccine;
KW    channel forming protein; junctional protein; conexin 32; ss.
XX
OS    Bos taurus.
XX
```

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FH    Key              Location/Qualifiers
FT    CDS              268. .3180
FT                     /*tag=  a
FT                     /product= "Bovine NCX-1 protein"
XX
PN    WO200206464-A2.
XX
PD    24-JAN-2002.
XX
PF    09-JUL-2001; 2001WO-US021606.
XX
PR    13-JUL-2000; 2000US-0218125P.
XX
PA    (UMOR ) UNIV MISSOURI.
XX
PI    Hale CC,  Price EM;
XX
DR    WPI; 2002-171806/22.
DR    P-PSDB; AAE18291.
XX
PT    Producing recombinant proteins e.g. membrane, transport and channel
PT    forming proteins in larvae expression system, by infecting larvae with
PT    vector having a sequence encoding recombinant fusion protein with
PT    affinity tag.
XX
PS    Example 1; Page 31-37; 40pp; English.
XX
CC    The patent discloses methods of producing recombinant proteins in larvae
CC    expression system, by infecting the larvae with vector having a sequence
CC    encoding recombinant fusion protein with affinity tag. The methods are
CC    useful for producing recombinant protein, preferably membrane proteins,
CC    transport proteins such as NCX1 (cardiac sodium-calcium exchange protein)
CC    or Na-K ATPase, channel forming proteins such as cystic fibrosis trans-
CC    membrane conductance regulator (CFTR), junctional protein (conexin 32),
CC    receptor, cytoskeletal and other membrane associated proteins. They are
CC    also useful for producing prostate specific membrane antigens and sodium
CC    phosphate co-transporters from kidney. The methods are also useful for
CC    producing recombinant fusion proteins in large quantities that are both
CC    highly homogenous and biologically active. The recombinant proteins
CC    produced by the methods of the invention can be included as part of a
CC    pharmaceutical, nutritional, drug or vaccine composition. The present
CC    sequence is a cDNA encoding bovine NCX-1 protein
XX
SQ    Sequence 4087 BP; 1057 A; 950 C; 1057 G; 1023 T; 0 U; 0 Other;

      Query Match               43.5%;   Score 810.6;   DB 6;   Length 4087;
      Best Local Similarity   68.5%;   Pred. No. 3.7e-242;
      Matches 1211;  Conservative    0;  Mismatches  519;  Indels   39;  Gaps    5;

Qy          46 TTTGGGCTGGTTACCTTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCA 105
               |||     || |  || | |||     || || |  | |  |   |     |||
Db         307 TTTCACGTGATAGCCATGGTGGCTCTCTTGTTTTCCCATGTGGACCATATAAGTGCTGAG 366

Qy         106 GGGGACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAG 165
               ||  ||  | |   ||| | | | ||    ||| | || || |   |||| |||
Db         367 ACAGAAATGGAAGGAGAAGGCAACGAGACTGGCGAGTGTACTGGCTCCTATTACTGTAAG 426
```

```
Qy    166 GAGGGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCC 225
          |||| || || | || || ||| | || || ||||||||| |||| ||||| |||||
Db    427 AAGGGGGTGATTTTACCCATTTGGGAGCCCCAGGACCCTTCCTTTGGAGACAAAATTGCT 486

Qy    226 AGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCT 285
          || | | ||| ||||||||||| || | |||||||| ||||| || || |||||||||
Db    487 AGAGCGACTGTGTATTTTGTGGCCATGGTCTACATGTTTCTTGGAGTCTCAATCATTGCT 546

Qy    286 GACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAG 345
          ||||| |||||| | |||||| ||||||||||| |||||||||| || | || || |||
Db    547 GACCGGTTCATGTCCTCTATAGAAGTCATCACGTCTCAAGAGAAAGAAATCACCATAAAG 606

Qy    346 AAACCCAATGGAGAAACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAAC 405
          |||||||||||||||| |||| || || ||| | || ||||||||| || || ||||||
Db    607 AAACCCAATGGAGAGACCACCAAGACAACTGTGAGGATCTGGAATGAGACAGTGTCCAAC 666

Qy    406 CTGACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTG 465
          |||||| | ||||||||||| || || ||||| ||||| |||||| || |||| ||||||
Db    667 CTGACCTTGATGGCCCTGGGGTCTTCAGCTCCAGAGATTCTCCTTTCAGTAATCGAGGTG 726

Qy    466 TGTGGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCC 525
          ||||| ||| |||| ||| || || || || ||| ||||| || |||||||| ||
Db    727 TGTGGCCATAACTTCACTGCAGGAGACCTTGGCCCTAGCACCATCGTGGGGAGTGCTGCA 786

Qy    526 TTCAACATGTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGC 585
          |||||||||||||||||||||||| | | |||||| || || |||| || || ||||| |
Db    787 TTCAACATGTTCATCATCATTGCCCTTTGTGTGTATGTCGTCCCGGATGGGGAGACAAGG 846

Qy    586 AAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATC 645
          ||||||||||||||| || || |||||| | || || || |||||| ||||||||||| |
Db    847 AAGATCAAGCATCTGCGTGTGTTCTTTGTGACAGCAGCATGGAGCATCTTTGCCTATACC 906

Qy    646 TGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTC 705
          ||||| || || ||| || | ||| ||||||||| |||||||| || ||||||||| |
Db    907 TGGCTTTACATCATTTTGTCTGTCAGCTCCCCTGGGGTCGTGGAGGTCTGGGAAGGTTTG 966

Qy    706 CTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTG 765
          || ||| ||||||||| || | || || | | || ||||||||||| | | ||
Db    967 CTTACTTTCTTCTTCTTCCCCATCTGCGTTGTGTTTGCTTGGGTGGCAGACAGGAGGCTT 1026

Qy    766 CTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATA 825
          || || |||||| || | |||| | ||| || | | ||| || | ||||| || ||
Db   1027 CTGTTTTACAAGTATGTCTACAAGAGGTATCGGGCTGGCAAGCAGAGGGGAATGATTATT 1086

Qy    826 GAGACAGAGGGTGACCACCC---------TAAGGGCATTGAGATGGATGGGAAAATGATG 876
          ||   || || ||| ||            | | ||||| ||||||||||||| || |
Db   1087 GAACACGAAGGAGACAGGCCATCTTCCAAGACAGAAATTGAAATGGATGGGAAAGTGGTC 1146

Qy    877 AATTCCCA---------TTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAG------ 921
          ||||||||         ||| ||||||| |||||| |||||| |    || |    ||
Db   1147 AATTCCCATGTTGACAGTTTCTTAGATGGAGCCCTGGTTCTGGAGGTTGATGAGAGGGAC 1206

Qy    922 ---GAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAA 978
             || | || || || | |||| ||| |||||||| |||||| || ||||| || |||
Db   1207 CAAGATGATGAAGAAGCCAGGCGAGAAATGGCTAGGATTCTGAAGGAACTCAAGCAGAAG 1266

Qy    979 CACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCAC 1038
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                 ||  ||||||||||||  ||||  ||   |   | ||   | ||||||||||  | |      |       ||
   Db   1267 CATCCAGAGAAGGAAATAGAGCAATTAATAGAATTAGCCAATTACCAAGTCTTAAGTCAG 1326

   Qy   1039 CAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGC 1098
                 ||  ||  ||  ||  ||  ||  ||  |||||||||  |||||  ||  ||   ||||||||  ||  ||||||
   Db   1327 CAGCAAAAAAGTCGAGCGTTTTACCGTATTCAAGCTACCCGCCTGATGACCGGAGCAGGC 1386

   Qy   1099 AATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTG 1158
                 ||  ||   |  ||||   ||||||||||||  |||||||  |||  ||    |||||||     |||||
   Db   1387 AACATTTTAAAGAGGCATGCAGCAGACCAAGCCAGGAAAGCTGTCAGCATGCATGAGGTC 1446

   Qy   1159 CACACCGATGAGCCTG---AGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTAC 1215
                 ||||  ||   |  |  |||    |  |||   ||  ||  ||  |||||||||||||||  |  |  |  |  | ||
   Db   1447 AACACGGAAGTGGCTGAAAATGACCCTGTCAGTAAGATCTTCTTTGAACAAGGGACATAT 1506

   Qy   1216 CAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATG 1275
                 |||||  ||||||||||||||||||  |  |||   |||||||  |   |   |  |  |||  ||  ||   ||
   Db   1507 CAGTGTCTGGAGAACTGTGGCACAGTAGCCCTGACCATTATCCGCAGAGGTGGTGATTTG 1566

   Qy   1276 TCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGAC 1335
                 |  ||  ||     |||  |||  ||||  ||  ||||||||||||||  |  |||||||||  ||     ||||
   Db   1567 ACCAACACTGTGTTTGTTGACTTCAGAACAGAGGATGGCACAGCCAATGCTGGATCTGAT 1626

   Qy   1336 TATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCC 1395
                 ||  ||  ||  ||  ||  ||  ||  ||  |||||   |  ||||||  ||  ||||||||||||||||   ||
   Db   1627 TACGAATTTACCGAAGGAACTGTGGTCTTTAAGCCTGGTGAGACCCAGAAGGAAATCAGA 1686

   Qy   1396 GTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGC 1455
                 ||  ||||||  ||||||||   ||||||  |||||||||||||||||||   |  |||  ||||       |  |||
   Db   1687 GTTGGCATCATTGATGATGACATCTTTGAGGAGGATGAGAATTTCCTTGTGCATCTCAGC 1746

   Qy   1456 AATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGT 1515
                 ||  |||      ||       |||       |  ||  ||  ||  ||  |       |||              ||||
   Db   1747 AACGTCAAAGTATCTTTGGAAGCCTCGGAAGACGGCATCCTGGAAGC---------CAGT 1797

   Qy   1516 CTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGAT 1575
                 |  |   ||     |  |    |||   |||  |  |||||  |        |||||  ||  ||  ||  ||  |||
   Db   1798 CATGTCTCTACCCTTGCTTGCCTGGGATCCCCCTCCACTGCCACCGTGACTATTTTTGAT 1857

   Qy   1576 GATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATT 1635
                 |||||||||||  ||||||||||  |||||||  ||||||||            |  ||||||  |||||||||  |||
   Db   1858 GATGACCATGCTGGCATCTTTACTTTTGAGGAACCGGTGACTCATGTGAGTGAGAGCATT 1917

   Qy   1636 GGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACAGTCATCGTCCCC 1695
                 ||   |  ||||||||||  ||  ||||||  |  |||||  ||  ||  ||  || |  ||  |||||||  |||
   Db   1918 GGCATCATGGAGGTGAAAGTTCTGAGAACATCTGGAGCACGTGGAAATGTTATCGTTCCC 1977

   Qy   1696 TTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGG 1755
                 |  ||  |||   |  ||  |||||  ||||  ||||  |||||  ||  ||||||||||||  |||||||   ||
   Db   1978 TATAAGACCATTGAGGGGACCGCCAGAGGTGGAGGGGAGGACTTTGAGGACACATGCGGA 2037

   Qy   1756 GAGTTGGAATTCAAGAATGATGAAACTGT 1784
                 ||| |  ||  |||  |||||||  ||||  |||
   Db   2038 GAGCTCGAGTTCCAGAATGACGAAATTGT 2066


   Search completed: June 25, 2004, 07:40:45
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Job time : 660.599 secs

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OM nucleic - nucleic search, using sw model

Run on: June 25, 2004, 06:15:36 ; Search time 142.069 Seconds
                                          (without alignments)
                                          7277.246 Million cell updates/sec

Title: US-10-054-680-3
Perfect score: 1863
Sequence: 1 atggcgtggttaaggttgca..........ggaaagccagtattgggtga 1863

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

| | | | %
Query | | | | |
Result	No.	Score	Match	Length	DB	ID	Description
	1	71.6	3.8	1935	4	US-09-701-068-3	Sequence 3, Appli
	2	71.6	3.8	1950	4	US-09-701-068-1	Sequence 1, Appli
	3	51.6	2.8	7218	1	US-08-232-463-14	Sequence 14, Appl
c	4	51	2.7	7218	1	US-08-232-463-14	Sequence 14, Appl
	5	44.8	2.4	2803	4	US-09-701-068-4	Sequence 4, Appli
	6	38.4	2.1	160	1	US-08-182-175A-44	Sequence 44, Appl
	7	38.4	2.1	160	1	US-08-474-633A-53	Sequence 53, Appl
	8	38.4	2.1	160	4	US-08-823-771-53	Sequence 53, Appl
	9	38.4	2.1	160	5	PCT-US92-06412-44	Sequence 44, Appl
c	10	38.4	2.1	2777	4	US-09-310-463-3	Sequence 3, Appli
c	11	38.4	2.1	2777	4	US-08-842-248A-3	Sequence 3, Appli

c	12	37.4	2.0	289	3	US-09-007-005-17	Sequence 17, Appl
c	13	37.4	2.0	289	3	US-09-244-796-17	Sequence 17, Appl
c	14	37.2	2.0	1320	4	US-09-148-545-110	Sequence 110, App
c	15	37	2.0	1890	3	US-08-935-855-19	Sequence 19, Appl
	16	36.8	2.0	160	1	US-08-182-175A-32	Sequence 32, Appl
	17	36.8	2.0	160	1	US-08-182-175A-34	Sequence 34, Appl
	18	36.8	2.0	160	1	US-08-474-633A-29	Sequence 29, Appl
	19	36.8	2.0	160	1	US-08-474-633A-31	Sequence 31, Appl
	20	36.8	2.0	160	4	US-08-823-771-29	Sequence 29, Appl
	21	36.8	2.0	160	4	US-08-823-771-31	Sequence 31, Appl
	22	36.8	2.0	160	5	PCT-US92-06412-32	Sequence 32, Appl
	23	36.8	2.0	160	5	PCT-US92-06412-34	Sequence 34, Appl
	24	36.8	2.0	187	1	US-08-182-175A-90	Sequence 90, Appl
	25	36.8	2.0	187	1	US-08-474-633A-78	Sequence 78, Appl
	26	36.8	2.0	187	4	US-08-823-771-78	Sequence 78, Appl
	27	36.8	2.0	187	5	PCT-US92-06412-90	Sequence 90, Appl
c	28	36.8	2.0	2790	3	US-08-985-950-21	Sequence 21, Appl
c	29	36.8	2.0	2790	4	US-09-546-049-21	Sequence 21, Appl
c	30	36.8	2.0	2922	4	US-09-310-463-1	Sequence 1, Appli
c	31	36.8	2.0	2922	4	US-08-842-248A-1	Sequence 1, Appli
	32	36.6	2.0	289	3	US-09-007-005-17	Sequence 17, Appl
	33	36.6	2.0	289	3	US-09-244-796-17	Sequence 17, Appl
	34	36	1.9	505	4	US-09-621-976-15639	Sequence 15639, A
c	35	36	1.9	1328	4	US-09-599-360B-46	Sequence 46, Appl
	36	35.6	1.9	189	3	US-09-461-697-213	Sequence 213, App
	37	35.6	1.9	195	3	US-09-461-697-211	Sequence 211, App
	38	35.6	1.9	213	3	US-09-461-697-209	Sequence 209, App
	39	35.6	1.9	231	3	US-09-461-697-207	Sequence 207, App
	40	35.6	1.9	282	3	US-09-461-697-205	Sequence 205, App
	41	35.6	1.9	306	3	US-09-461-697-203	Sequence 203, App
	42	35.6	1.9	696	3	US-09-461-697-193	Sequence 193, App
	43	35.6	1.9	699	3	US-09-461-697-191	Sequence 191, App
	44	35.6	1.9	717	3	US-09-461-697-189	Sequence 189, App
	45	35.6	1.9	774	3	US-09-461-697-187	Sequence 187, App

ALIGNMENTS

RESULT 1
US-09-701-068-3
; Sequence 3, Application US/09701068
; Patent No. 6677506
; GENERAL INFORMATION:
;   APPLICANT: Galil, Gad et al.
;   TITLE OF INVENTION: DNA CODING FOR A Mg2+/H+ OR Zn2+/H+ EXCHANGER AND
TRANSGENIC PLANTS
;   TITLE OF INVENTION: EXPRESSING SAME
;   FILE REFERENCE: 01/21317
;   CURRENT APPLICATION NUMBER: US/09/701,068
;   CURRENT FILING DATE: 2001-05-07
;   NUMBER OF SEQ ID NOS: 17
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 1935
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana

   Query Match   3.8%;   Score 71.6;   DB 4;   Length 1935;
   Best Local Similarity   48.2%;   Pred. No. 4.8e-12;
   Matches 268; Conservative   0; Mismatches 279; Indels   9; Gaps   2;

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Qy     226 AGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCT 285
           ||||    |  | |||||| | |  ||     ||| |  ||||| |||| | ||| ||
Db     253 AGGGGTGTGTTATATTTTCTCGGTCTTGCCTACTGCTTTATTGGGTTGTCAGCCATCACT 312

Qy     286 GACCGCTTCATGGCATCTATTG---AAGTCATCACCTCTCAAGAGAGGGAGGTGACAATT 342
           |  || ||| |      ||||| | ||| | |    |      | |  ||| ||||||
Db     313 GCACGGTTCTTCAAGTCTATGGAGAATGTCGTGAAACATTCCCGTAAAGTGGTTACAATT 372

Qy     343 AAGAAACCCAATGGAGAAACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCC 402
            |        | |  ||        ||  ||   |      || |||||    ||| |  |
Db     373 GATCCCATTACTAAAGCTGAAGTCATCACATACAAGAAAGTTTGGAACTTTACTATTGCA 432

Qy     403 AACCTGACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAG 462
            || | |  |  |||| | ||  |  |       ||| ||||      | ||   || ||
Db     433 GACATCAGTTTGTTGGCGTTTGGAACTAGCTTCCCTCAGATTTCTTTGGCTACCATCGAT 492

Qy     463 GTGTGTGGTCAT------GGGTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGG 516
           |     | ||      |  |      |||||| | ||| || |||   || |||| ||
Db     493 GCAATACGGAATATGGGGGAGCGGTATGCTGGAGGTCTTGGTCCTGGAACACTTGTTGGC 552

Qy     517 AGTGCAGCCTTCAACATGTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGA 576
             || || ||  |  | ||  |||| |   | ||||||    |  | ||   ||  |||
Db     553 TCAGCTGCATTTGATCTTTTCCCCATCCACGCTGTTTGTGTCGTTGTGCCAAAAGCTGGA 612

Qy     577 GAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTT 636
           ||        |||||       |  || | ||  |   |  |        | ||| | | |
Db     613 GAACTGAAAAAGATATCCGACTTAGGTGTTTGGCTAGTTGAGCTCGTATGGTCTTTTTGG 672

Qy     637 GCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGG 696
           || |||||||||||| || || || || |  || |  || || ||     || |   || |
Db     673 GCTTACATCTGGCTATACATAATCCTCGAGGTGTGGTCACCAAACGTAATTACACTTGTG 732

Qy     697 GAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGAT 756
           || |   |   | || |  |    |   |  | || || ||| || |  |      |||
Db     733 GAGGCATTATTGACAGTACTGCAATACGGATTGCTTCTAGTTCATGCGTACGCCCAAGAC 792

Qy     757 AAACGACTGCTCTTCT 772
           || |||  ||  | ||
Db     793 AAGCGATGGCCTTACT 808
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; TITLE OF INVENTION: DNA CODING FOR A Mg2+/H+ OR Zn2+/H+ EXCHANGER AND
TRANSGENIC PLANTS
; TITLE OF INVENTION: EXPRESSING SAME
; FILE REFERENCE: 01/21317
; CURRENT APPLICATION NUMBER: US/09/701,068
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1950
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-701-068-1

    Query Match   3.8%;   Score 71.6; DB 4;   Length 1950;
    Best Local Similarity   48.2%;   Pred. No. 4.8e-12;
    Matches 268; Conservative   0; Mismatches 279; Indels   9; Gaps   2;

Qy   226 AGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCT 285
                |||| | | ||||||| || || ||| || ||||| |||| ||| ||
Db   258 AGGGGTGTGTTATATTTTCTCGGTCTTGCCTACTGCTTTATTGGGTTGTCAGCCATCACT 317

Qy   286 GACCGCTTCATGGCATCTATTG---AAGTCATCACCTCTCAAGAGAGGGAGGTGACAATT 342
                | || ||| | |||||| | | ||| | | | | ||| ||||||
Db   318 GCACGGTTCTTCAAGTCTATGGAGAATGTCGTGAAACATTCCCGTAAAGTGGTTACAATT 377

Qy   343 AAGAAACCCAATGGAGAAACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCC 402
                | | | || || || | || |||||| ||| | |
Db   378 GATCCCATTACTAAAGCTGAAGTCATCACATACAAGAAAGTTTGGAACTTTACTATTGCA 437

Qy   403 AACCTGACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAG 462
                || | | | |||| | || | ||| |||| | || || ||
Db   438 GACATCAGTTTGTTGGCGTTTGGAACTAGCTTCCCTCAGATTTCTTTGGCTACCATCGAT 497

Qy   463 GTGTGTGGTCAT------GGGTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGG 516
                | | || || || |||||| | ||| || ||| || |||| ||
Db   498 GCAATACGGAATATGGGGGAGCGGTATGCTGGAGGTCTTGGTCCTGGAACACTTGTTGGC 557

Qy   517 AGTGCAGCCTTCAACATGTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGA 576
                || || || | | ||| |||| | | || |||||| ||| || |||
Db   558 TCAGCTGCATTTGATCTTTTCCCCATCCACGCTGTTTGTGTCGTTGTGCCAAAAGCTGGA 617

Qy   577 GAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTT 636
                || ||||| | || | || | | | | ||| | | |
Db   618 GAACTGAAAAAGATATCCGACTTAGGTGTTTGGCTAGTTGAGCTCGTATGGTCTTTTTGG 677

Qy   637 GCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGG 696
                || |||||||||| || || || || | || | || || || | || |
Db   678 GCTTACATCTGGCTATACATAATCCTCGAGGTGTGGTCACCAAACGTAATTACACTTGTG 737

Qy   697 GAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGAT 756
                || | | | | || | | | ||| || || ||| ||| ||| | |||
Db   738 GAGGCATTATTGACAGTACTGCAATACGGATTGCTTCTAGTTCATGCGTACGCCCAAGAC 797

Qy   757 AAACGACTGCTCTTCT 772
                || ||| || | ||
Db   798 AAGCGATGGCCTTACT 813

RESULT 3
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
;   APPLICANT: DORNER, F.
;   APPLICANT: SCHEIFLINGER, F.
;   APPLICANT: FALKNER, F. G.
;   TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
;   NUMBER OF SEQUENCES: 52
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Foley & Lardner
;   STREET: 1800 Diagonal Road, Suite 500
;   CITY: Alexandria
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22313-0299
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/232,463
;   FILING DATE:
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/07/935,313
;   FILING DATE:
;   APPLICATION NUMBER: EP 91 114 300.6
;   FILING DATE: 26-AUG-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: BENT, Stephen A.
;   REGISTRATION NUMBER: 29,768
;   REFERENCE/DOCKET NUMBER: 30472/114 IMMU
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (703)836-9300
;   TELEFAX: (703)683-4109
;   TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 7218 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   IMMEDIATE SOURCE:
;   CLONE: pTZgpt-Fls
US-08-232-463-14

   Query Match   2.8%; Score 51.6; DB 1; Length 7218;
   Best Local Similarity 5.9%; Pred. No. 2.7e-05;
   Matches   24; Conservative 215; Mismatches 169; Indels   0; Gaps   0;

Qy   395 CTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTT 454
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Db     1078  YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1137

Qy      455  TAATTGAGGTGTGTGGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAG 514
             :  ::     :  :  :   ::  :    :::  :: ::   :  :::     ::::::: :: :: :
Db     1138  YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1197

Qy      515  GGAGTGCAGCCTTCAACATGTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACG 574
             :  :   :::::: :  :  ::: :: ::  ::   :  :::  :  ::: : :  ::::    :
Db     1198  YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1257

Qy      575  GAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCT 634
             ::: :     ::    : ::: :   :::::::::: :: :: ::  :::     : :::
Db     1258  YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1317

Qy      635  TTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTT 694
             :: :::  : :::   :::: : :    :::: :    :::::::::::::  : :   :::     :::
Db     1318  YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1377

Qy      695  GGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAG 754
             :::::::: :::::::::::::::::::::   : : : ::::::::   :::        :
Db     1378  YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYGTA 1437

Qy      755  ATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAG 802
             |||    |      |||  || |||  ||||  |  | ||       ||||
Db     1438  CCAAATTCTTCTATCTCTTTAACTACTTGCATAGATAGGTAATTACAG 1485
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RESULT 4
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
;   GENERAL INFORMATION:
;   APPLICANT: DORNER, F.
;   APPLICANT: SCHEIFLINGER, F.
;   APPLICANT: FALKNER, F. G.
;   TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
;   NUMBER OF SEQUENCES: 52
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Foley & Lardner
;   STREET: 1800 Diagonal Road, Suite 500
;   CITY: Alexandria
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22313-0299
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/232,463
;   FILING DATE:
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/07/935,313
;   FILING DATE:
;   APPLICATION NUMBER: EP 91 114 300.6

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  Query Match              2.7%;  Score 51;  DB 1;  Length 7218;
  Best Local Similarity  3.4%;  Pred. No. 4.2e-05;
  Matches    9;  Conservative  161;  Mismatches   91;  Indels   0;  Gaps    0;


Qy      1603 GAATGTGATACTATTCATGTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGG 1662
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Db      1445 GAATTTGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1386


Qy      1663 ACATCAGGTGCCCGGGGGTACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAG 1722
             : : ::: :   :::: : :: : :      :::: :: :::::::: :: :::
Db      1385 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1326


Qy      1723 GGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACT 1782
             :: :: :: :::::      :::::: : : : ::::::  ::::    ::::: :: ::::
Db      1325 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1266


Qy      1783 GTATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGAT 1842
             : : : :: ::: :::::: :: : ::::::::::::::::  ::::::: :: :::::
Db      1265 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1206


Qy      1843 GGGAAAGCCAGTATTGGGTGA 1863
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Db      1205 RRRRRRRRRRRRRRRRRRRRR 1185



RESULT 5
US-09-701-068-4
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 2803
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-701-068-4

  Query Match   2.4%;   Score 44.8; DB 4;   Length 2803;
  Best Local Similarity 52.1%; Pred. No. 0.0021;
  Matches 100; Conservative   0; Mismatches 92; Indels   0; Gaps   0;

Qy   477 GTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTT 536
              ||| | | | ||| || ||| || |||| || || || || | | ||
Db   950 GTTTTGTCATATAGGTCTTGGTCCTGGAACACTTGTTGGCTCAGCTGCATTTGATCTTTT 1009

Qy   537 CATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCA 596
              | |||| | | |||||| ||| || ||||| ||||| |
Db   1010 CCCCATCCACGCTGTTTGTGTCGTTGTGCCAAAAGCTGGAGAACTGAAAAAGATATCCGA 1069

Qy   597 TCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATAT 656
              || | || | | | | ||| | | || |||||||||||| || ||
Db   1070 CTTAGGTGTTTGGCTAGTTGAGCTCGTATGGTCTTTTTGGGCTTACATCTGGCTATACAT 1129

Qy   657 GATTCTGGCAGT 668
              || || | ||
Db   1130 AATCCTCGAGGT 1141

RESULT 6
US-08-182-175A-44
; Sequence 44, Application US/08182175A
; Patent No. 5559223
; GENERAL INFORMATION:
;   APPLICANT: Saverio Carl Falco
;   APPLICANT: Sharon J. Keeler
;   APPLICANT: Janet A. Rice
;   TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure
Containing Pro
;   NUMBER OF SEQUENCES: 113
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: E.I. du Pont de Nemours and Company
;   STREET: 1007 Market Street
;   CITY: Wilmington
;   STATE: Delaware
;   COUNTRY: USA
;   ZIP: 19898
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy Disk
;   COMPUTER: Macintosh
;   OPERATING SYSTEM: Macintosh System, 6.0
;   SOFTWARE: Microsoft Word, 4.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/182,175A
;   FILING DATE:
;   CLASSIFICATION: 800
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/743,006

;   INFORMATION FOR SEQ ID NO: 44:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 160 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   ORIGINAL SOURCE:
;   STRAIN: E. coli
;   CELL TYPE: DH5 alpha
;   IMMEDIATE SOURCE:
;   CLONE: 82-4
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 2..151
;   OTHER INFORMATION: /function= "synthetic storage protein
;   OTHER INFORMATION: /product= "protein"
;   OTHER INFORMATION: /gene= "ssp"
;   OTHER INFORMATION: /standard_name= "7.7.7.7.7.7.5"
US-08-182-175A-44

   Query Match   2.1%; Score 38.4; DB 1; Length 160;
   Best Local Similarity   53.3%; Pred. No. 0.032;
   Matches   81; Conservative   0; Mismatches   71; Indels   0; Gaps   0;

Qy   1708 GAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAATTC 1767
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   4 GGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGC 63

Qy   1768 AAGAATGATGAAACTGTATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAA 1827
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   64 GATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAA 123

Qy   1828 GAGGATAGCAGAGATGGGAAAGCCAGTATTGG 1859
             | | | | | | | | | | | | | | | | | | | | |
Db   124 GGCGATGGAAGAGAAGATGAAGGCGTGATAGG 155

RESULT 7
US-08-474-633A-53
; Sequence 53, Application US/08474633A
; Patent No. 5773691
;   GENERAL INFORMATION:
;   APPLICANT: E. I. DU PONT DE NEMOURS AND
;   APPLICANT: COMPANY
;   TITLE OF INVENTION: CHIMERIC GENES AND
;   TITLE OF INVENTION: METHODS FOR INCREASING
;   TITLE OF INVENTION: INCREASING THE LYSINE

```
;     TITLE OF INVENTION:  AND THREONINE CONTENT
;     TITLE OF INVENTION:  OF THE SEEDS OF PLANTS
;     NUMBER OF SEQUENCES:  107
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  E. I. DU PONT DE NEMOURS
;       ADDRESSEE:  AND COMPANY
;       STREET:  1007 MARKET STREET
;       CITY:  WILMINGTON
;       STATE:  DELAWARE
;       COUNTRY:  U.S.A.
;       ZIP:  19898
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  FLOPPY DISK
;       COMPUTER:  IBM PC COMPATIBLE
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  MICROSOFT WORD VERSION 2.0C
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/474,633A
;       FILING DATE:
;       CLASSIFICATION:  800
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  BARBARA C. SIEGELL
;       REGISTRATION NUMBER:  30,684
;       REFERENCE/DOCKET NUMBER:  BB-1037-C
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  302-992-4931
;       TELEFAX:  302-773-0164
;       TELEX:  835420
;   INFORMATION FOR SEQ ID NO:  53:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  160 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     ORIGINAL SOURCE:
;       STRAIN:  E. coli
;       CELL TYPE:  DH5 alpha
;     IMMEDIATE SOURCE:
;       CLONE:  82-4
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  2..151
;       OTHER INFORMATION:  /function= "synthetic
;       OTHER INFORMATION:  storage protein
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;       OTHER INFORMATION:  "7.7.7.7.7.7.5"
US-08-474-633A-53

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   Matches   81;  Conservative   0;  Mismatches  71;  Indels   0;  Gaps   0;

Qy     1708 GAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAATTC 1767
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Qy      1768  AAGAATGATGAAACTGTATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAA  1827
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RESULT 8
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; Sequence 53, Application US/08823771
; Patent No. 6459019
;   GENERAL INFORMATION:
;   APPLICANT: E. I. DU PONT DE NEMOURS AND
;   COMPANY
;   TITLE OF INVENTION: CHIMERIC GENES AND
;   METHODS FOR INCREASING
;   INCREASING THE LYSINE
;   AND THREONINE CONTENT
;   NUMBER OF SEQUENCES: 107
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: E. I. DU PONT DE NEMOURS
;   AND COMPANY
;   STREET: 1007 MARKET STREET
;   CITY: WILMINGTON
;   STATE: DELAWARE
;   COUNTRY: U.S.A.
;   ZIP: 19898
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: FLOPPY DISK
;   COMPUTER: IBM PC COMPATIBLE
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: MICROSOFT WORD VERSION 2.0C
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/823,771
;   FILING DATE: 24-Mar-1997
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/474,633
;   FILING DATE: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;   NAME: BARBARA C. SIEGELL
;   REGISTRATION NUMBER: 30,684
;   REFERENCE/DOCKET NUMBER: BB-1037-C
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 302-992-4931
;   TELEFAX: 302-773-0164
;   TELEX: 835420
;   INFORMATION FOR SEQ ID NO: 53:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 160 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
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Qy      1768 AAGAATGATGAAACTGTATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAA 1827
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Db        64 GATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAA 123


Qy      1828 GAGGATAGCAGAGATGGGAAAGCCAGTATTGG 1859
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Db       124 GGCGATGGAAGAGAAGATGAAGGCGTGATAGG 155
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RESULT 9
PCT-US92-06412-44

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Db         4 GGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGC 63


Qy      1768 AAGAATGATGAAACTGTATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAA 1827
               |    |   ||| ||| | | || || ||||||||    | || ||| ||    ||
Db        64 GATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAA 123


Qy      1828 GAGGATAGCAGAGATGGGAAAGCCAGTATTGG 1859
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Db       124 GGCGATGGAAGAGAAGATGAAGGCGTGATAGG 155
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RESULT 10
US-09-310-463-3/c
; Sequence 3, Application US/09310463A
; Patent No. 6384203

US-09-310-463-3

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Db       280 ACAGAGCCTGGTTCAGCCCAGAGGGTGGGCTTGGGGAGGTGCCCTGCCTGCACGTGGGTC 221


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RESULT 11
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Qy    1363 CTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTT 1422
           |||  |||  ||   | || || || ||  | |        |  | || ||     |  |
Db     220 CTGGGGCCCAGACTCAGCCCGAGACAGATCAGGACCGTGAGGATGGGGGTCATGGCGTCT 161

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             ::: : ::: : :: : :     :  :     ::: : ::: :   :|: : : :
Db       105 YSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYCYAYTYTYGYT 46


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;   EARLIER APPLICATION NUMBER: 60/040,162
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;   EARLIER APPLICATION NUMBER: 60/056,864
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;   EARLIER APPLICATION NUMBER: 60/043,578
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;   EARLIER APPLICATION NUMBER: 60/056,876
;   EARLIER FILING DATE: 1997-08-22
;   EARLIER APPLICATION NUMBER: 60/056,881
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Qy   614 TCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCT 673
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Db   750 TCCCGGCTGCCAGGGCTCACTTCCAAGCTTACAGAACTCGTGTCACTCATTGTGTCAGCT 691

Qy   674 CCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTG 733
              || || | || || | | |||||||| || | | |||||| | |||
Db   690 CCTGTGCCATCCACCTGGGTGTCAATGGCCTCCACAAGCCCCCGCCATTTCCACTCTGTC 631

Qy   734 TCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTA 773
              |||||| | || ||| |||| :| | |
Db   630 TCCTTCATCTCAGGCACATAGAAGTCTCCCTGCCSTGCCA 591

RESULT 15
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; Sequence 19, Application US/08935855
; Patent No. 6066485
;   GENERAL INFORMATION:
;   APPLICANT: Guthridge, Mark
;   APPLICANT: Basilico, Claudio
;   TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
;   TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
;   NUMBER OF SEQUENCES: 22
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: David A. Jackson, Esq.
;   STREET: 411 Hackensack Ave, Continental Plaza, 4th
;   STREET: Floor

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  Query Match                2.0%;  Score 37;  DB 3;  Length 1890;
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  Matches   76;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;


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Qy      702 CCTCCTCACTCTCTTCTTCTT 722
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2004, 07:13:27 ; Search time 753.008 Seconds
                                            (without alignments)
                                            11333.972 Million cell updates/sec

Title: US-10-054-680-3
Perfect score: 1863
Sequence: 1 atggcgtggttaaggttgca..........ggaaagccagtattgggtga 1863

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
                  1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                  2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                  3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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                  19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query

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      No.   Score  Match  Length DB   ID                      Description
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        1   1863   100.0   1863   14   US-10-054-680-3          Sequence 3, Appli
        2   1784.6  95.8   2766   14   US-10-054-680-1          Sequence 1, Appli
        3   1784.6  95.8   3812   14   US-10-054-680-5          Sequence 5, Appli
        4   1784.4  95.8   2534   15   US-10-256-537-1          Sequence 1, Appli
        5   1784.4  95.8   2534   15   US-10-256-537-3          Sequence 3, Appli
        6   1783    95.7   2781   15   US-10-275-116-1          Sequence 1, Appli
        7   1783    95.7   2782    9   US-09-804-474A-1         Sequence 1, Appli
        8   1782.8  95.7 126512    9   US-09-804-474A-3         Sequence 3, Appli
        9   1782.4  95.7   2813   15   US-10-114-153-1          Sequence 1, Appli
       10   1782.4  95.7   2840   15   US-10-114-153-3          Sequence 3, Appli
       11   1694.8  91.0   2685   15   US-10-114-153-5          Sequence 5, Appli
       12   821.4   44.1    823   15   US-10-029-386-20265      Sequence 20265, A
       13   810.6   43.5   4087    9   US-09-901-419-1          Sequence 1, Appli
       14   785.2   42.1   1836    9   US-09-864-761-16939      Sequence 16939, A
       15   783.2   42.0   6106   16   US-10-062-674-1648       Sequence 1648, Ap
       16   713.4   38.3   3004   16   US-10-388-934-506        Sequence 506, App
       17   692.4   37.2   4282   15   US-10-281-866-1          Sequence 1, Appli
       18   692.4   37.2   4282   15   US-10-281-866-3          Sequence 3, Appli
       19   503.4   27.0    505   15   US-10-029-386-6536       Sequence 6536, Ap
       20   494     26.5    551   15   US-10-029-386-4103       Sequence 4103, Ap
       21   366     19.6    366   15   US-10-029-386-17804      Sequence 17804, A
       22   334.4   17.9    507   15   US-10-029-386-4003       Sequence 4003, Ap
       23   180      9.7    180   15   US-10-029-386-17706      Sequence 17706, A
       24   164.2    8.8    459    9   US-09-864-761-102        Sequence 102, App
       25   146.6    7.9   1132   16   US-10-369-493-30006      Sequence 30006, A
       26   91.4     4.9   1792   16   US-10-369-493-29835      Sequence 29835, A
       27   79       4.2    477   10   US-09-918-995-2005       Sequence 2005, Ap
       28   79       4.2   1187   13   US-10-243-552-809        Sequence 809, App
       29   71.6     3.8   1617    9   US-09-938-842A-2591      Sequence 2591, Ap
       30   71.6     3.8   1617   11   US-09-938-842A-2591      Sequence 2591, Ap
       31   58.2     3.1    862   13   US-10-424-599-86000      Sequence 86000, A
       32   39.6     2.1   1635   13   US-10-282-122A-29169     Sequence 29169, A
       33   39.6     2.1  30306   13   US-10-087-192-523        Sequence 523, App
       34   38.6     2.1    750   13   US-10-027-632-18725      Sequence 18725, A
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       36   38.4     2.1    160   15   US-10-023-066A-53        Sequence 53, Appl
  c    37   38.4     2.1   2777   15   US-10-139-662-3          Sequence 3, Appli
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  c    40   38.4     2.1   2897   13   US-10-240-425-366        Sequence 366, App
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       42   37.8     2.0   1638   13   US-10-282-122A-29556     Sequence 29556, A
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  c    44   37.4     2.0   2946   16   US-10-369-493-33761      Sequence 33761, A
       45   37.2     2.0    903   13   US-10-424-599-131200     Sequence 131200,
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ALIGNMENTS

RESULT 1
US-10-054-680-3
; Sequence 3, Application US/10054680
; Publication No. US20020132998A1
; GENERAL INFORMATION:

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   Query Match              100.0%;  Score 1863;  DB 14;  Length 1863;
   Best Local Similarity    100.0%;  Pred. No. 0;
   Matches 1863;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


Qy         1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy        61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy       121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Db       121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy       181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy       241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300

Qy       301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Db       301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy       361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Db       361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy       421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db       421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy       481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Db       481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Qy    541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Db    541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

Qy    601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Qy    661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Db    661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

Qy    721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Qy    781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Qy    841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Db    901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960

Qy    961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020

Qy   1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Db   1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080

Qy   1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Qy   1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
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Db   1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260

Qy   1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320

Qy   1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Db   1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Qy    1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Qy    1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Qy    1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Db    1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560

Qy    1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Db    1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680

Qy    1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy    1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
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Db    1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800

Qy    1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGG 1860
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Qy    1861 TGA 1863
           |||
Db    1861 TGA 1863
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RESULT 2
US-10-054-680-1
; Sequence 1, Application US/10054680
; Publication No. US20020132998A1
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. US20020132998A1el Human Ion Exchanger Proteins and
Polynucleotides Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0301-USA
; CURRENT APPLICATION NUMBER: US/10/054,680
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/263,384
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 2766
;   TYPE: DNA

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    Best Local Similarity      98.5%;   Pred. No. 0;
    Matches 1813;  Conservative    0;  Mismatches   24;  Indels    4;  Gaps     1;
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Db         1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy        61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy       121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Qy       181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db       181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy       241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Qy       301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Qy       361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Db       361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy       421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Qy       481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Db       481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540

Qy       541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Db       541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

Qy       601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Db       601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660

Qy       661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Db       661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

Qy       721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Db       721  TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC  780

Qy       781  ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC  840
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Db       781  ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC  840

Qy       841  CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC  900
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Db       841  CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC  900

Qy       901  CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC  960
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Db       901  CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC  960

Qy       961  AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT  1020
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Db       961  AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT  1020

Qy      1021  TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT  1080
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Db      1021  TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT  1080

Qy      1081  ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC  1140
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Db      1081  ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC  1140

Qy      1141  TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT  1200
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Db      1141  TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT  1200

Qy      1201  GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG  1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201  GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG  1260

Qy      1261  AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC  1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261  AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC  1320

Qy      1321  AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC  1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321  AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC  1380

Qy      1381  CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC  1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381  CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC  1440

Qy      1441  TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA  1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441  TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA  1500

Qy      1501  GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA  1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501  GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA  1560

Qy      1561  GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT  1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561  GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT  1620
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Qy      1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680

Qy      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
             ||||||||||||||||||||||||||||||||||||||||||     ||||| |  || |
Db      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1796

Qy      1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
             | | |  || | ||| |||||||   |    |    |||||
Db      1797 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837


RESULT 3
US-10-054-680-5
; Sequence 5, Application US/10054680
; Publication No. US20020132998A1
; GENERAL INFORMATION:
;  APPLICANT: Friddle, Carl Johan
;  APPLICANT:  Hilbun, Erin
;  TITLE OF INVENTION: No. US20020132998A1el Human Ion Exchanger Proteins and
Polynucleotides Encoding the
;  TITLE OF INVENTION:   Same
;  FILE REFERENCE: LEX-0301-USA
;  CURRENT APPLICATION NUMBER: US/10/054,680
;  CURRENT FILING DATE:   2002-01-22
;  PRIOR APPLICATION NUMBER: US 60/263,384
;  PRIOR FILING DATE: 2001-01-23
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 3812
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-054-680-5

    Query Match          95.8%;  Score 1784.6;  DB 14;  Length 3812;
    Best Local Similarity  98.5%;  Pred. No. 0;
    Matches 1813;  Conservative   0;  Mismatches   24;  Indels   4;  Gaps    1;

Qy         1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       618 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 677

Qy        61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       678 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 737

Qy       121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       738 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 797
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Qy    181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    798 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 857

Qy    241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    858 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 917

Qy    301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    918 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 977

Qy    361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    978 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 1037

Qy    421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1038 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 1097

Qy    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1098 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 1157

Qy    541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1158 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 1217

Qy    601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1218 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1277

Qy    661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1278 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1337

Qy    721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1338 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1397

Qy    781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1398 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 1457

Qy    841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1458 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 1517

Qy    901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1518 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1577

Qy    961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1578 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1637

Qy   1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1638 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1697

Qy   1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1698 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1757

Qy   1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1758 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1817

Qy   1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1818 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1877

Qy   1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1878 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1937

Qy   1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1938 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1997

Qy   1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1998 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 2057

Qy   1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2058 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 2117

Qy   1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2118 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 2177

Qy   1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2178 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 2237

Qy   1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2238 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 2297

Qy   1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2298 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2357

Qy   1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
                   ||||||||||||||||||||||||||||||||||||||||||    |||||  |   ||  |
Db   2358 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 2413

Qy   1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
                   |  |  |   || |  | |||  |||||||||    |      |   |||||
Db   2414 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 2454
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RESULT 4

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     Query Match              95.8%;   Score 1784.4;   DB 15;   Length 2534;
     Best Local Similarity    99.9%;   Pred. No. 0;
     Matches 1785;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;


Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 402


Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 462


Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 522


Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        523 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 582


Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        583 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 642


Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        643 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 702


Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              ||||||||||||||||||||||||||·||||||||||||||||||||||||||||||||||
Db        703 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 762


Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        763 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 822


Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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                   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      823 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 882

Qy      541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
                   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      883 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 942

Qy      601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
                   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      943 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1002

Qy      661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
                   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1003 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1062

Qy      721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
                   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1063 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1122

Qy      781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
                   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1123 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 1182

Qy      841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
                   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1183 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 1242

Qy      901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
                   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1243 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1302

Qy      961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
                   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1303 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1362

Qy     1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
                   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1363 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1422

Qy     1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
                   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1423 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1482

Qy     1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
                   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1483 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1542

Qy     1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
                   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1543 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1602

Qy     1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
                   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1603 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1662

Qy     1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
                   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Db      1663 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1722

Qy      1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1723 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1782

Qy      1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1783 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1842

Qy      1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1843 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1902

Qy      1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1903 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1962

Qy      1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1963 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 2022

Qy      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2023 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2082

Qy      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
             ||||||||||||||||||||||||||||||||||||||||||||| |
Db      2083 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGT 2128
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RESULT 5
US-10-256-537-3
; Sequence 3, Application US/10256537
; Publication No. US20030162196A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; TITLE OF INVENTION: METHODS OF USING 69039, A NOVEL HUMAN
; TITLE OF INVENTION: NA/CA EXCHANGER FAMILY MEMBER
; FILE REFERENCE: MPI01-231P1RM
; CURRENT APPLICATION NUMBER: US/10/256,537
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/325,737
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2534
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (343)...(2130)
US-10-256-537-3

  Query Match   95.8%;   Score 1784.4; DB 15; Length 2534;
  Best Local Similarity 99.9%;   Pred. No. 0;

Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    343 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 402

Qy     61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    403 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 462

Qy    121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    463 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 522

Qy    181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    523 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 582

Qy    241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    583 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 642

Qy    301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    643 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 702

Qy    361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    703 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 762

Qy    421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    763 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 822

Qy    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    823 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 882

Qy    541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    883 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 942

Qy    601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    943 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1002

Qy    661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1003 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1062

Qy    721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1063 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1122

Qy    781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1123 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 1182
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Qy    841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1183 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 1242

Qy    901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1243 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1302

Qy    961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1303 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1362

Qy   1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1363 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1422

Qy   1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1423 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1482

Qy   1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1483 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1542

Qy   1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1543 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1602

Qy   1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1603 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1662

Qy   1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1663 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1722

Qy   1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1723 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1782

Qy   1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1783 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1842

Qy   1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1843 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1902

Qy   1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1903 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1962

Qy   1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1963 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 2022
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Qy      1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2023 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2082

Qy      1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
             ||||||||||||||||||||||||||||||||||||||||||||| |
Db      2083 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGT 2128
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RESULT 6
US-10-275-116-1
; Sequence 1, Application US/10275116
; Publication No. US20030096312A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; TITLE OF INVENTION: No. US20030096312A1el natrium-calium exchanger protein
; FILE REFERENCE: HNCX3CWWS
; CURRENT APPLICATION NUMBER: US/10/275,116
; CURRENT FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2781
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2781)
US-10-275-116-1

  Query Match   95.7%; Score 1783; DB 15; Length 2781;
  Best Local Similarity   98.4%; Pred. No. 0;
  Matches 1812; Conservative   0; Mismatches   25; Indels   4; Gaps   1;

Qy   1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy   61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy   121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy   181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy   241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300

Qy   301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Qy    361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy    421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540

Qy    541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

Qy    601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660

Qy    661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

Qy    721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780

Qy    781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840

Qy    841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900

Qy    901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960

Qy    961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020

Qy   1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
          ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db   1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGTGCCTTCTACCGTATCCAAGCCACTCGT 1080

Qy   1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140

Qy   1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Qy    1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260

Qy    1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320

Qy    1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

Qy    1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440

Qy    1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

Qy    1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560

Qy    1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620

Qy    1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680

Qy    1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy    1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
           |||||||||||||||||||||||||||||||||||||||||     |||||  |  || |
Db    1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1796

Qy    1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
           |  |  || | ||| |||||||    |    ||||||
Db    1797 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837
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RESULT 7
US-09-804-474A-1
; Sequence 1, Application US/09804474A
; Patent No. US20020119518A1
; GENERAL INFORMATION:
; APPLICANT: KODET, Stefan et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER
PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000891
; CURRENT APPLICATION NUMBER: US/09/804,474A

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Query Match            95.7%;  Score 1783;  DB 9;  Length 2782;
Best Local Similarity  98.4%;  Pred. No. 0;
Matches 1812;  Conservative   0;  Mismatches  25;  Indels   4;  Gaps   1;


Qy        1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       10 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 69


Qy       61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       70 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 129


Qy      121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      130 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 189


Qy      181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      190 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 249


Qy      241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      250 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 309


Qy      301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      310 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 369


Qy      361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      370 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 429


Qy      421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      430 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 489


Qy      481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      490 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 549


Qy      541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      550 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 609


Qy      601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      610 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 669
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Qy       661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       670 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 729

Qy       721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       730 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 789

Qy       781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       790 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 849

Qy       841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       850 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 909

Qy       901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db       910 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATCCTC 969

Qy       961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       970 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1029

Qy      1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1030 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1089

Qy      1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1090 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1149

Qy      1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1150 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1209

Qy      1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1210 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1269

Qy      1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1270 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1329

Qy      1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1330 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1389

Qy      1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1390 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1449

Qy      1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1450 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1509

Qy      1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1510  GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1569

Qy      1561  GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1570  GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1629

Qy      1621  GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1630  GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1689

Qy      1681  ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1690  ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1749

Qy      1741  GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
              |||||||||||||||||||||||||||||||||||||||||||   |||||  |  ||  |
Db      1750  GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1805

Qy      1801  GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
              | | |  || | ||| |||||||    |    | |||||
Db      1806  GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1846


RESULT 8
US-09-804-474A-3
; Sequence 3, Application US/09804474A
; Patent No. US20020119518A1
; GENERAL INFORMATION:
;  APPLICANT: KODET, Stefan et al
;  TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER
PROTEINS,
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: CL000891
;  CURRENT APPLICATION NUMBER: US/09/804,474A
;  CURRENT FILING DATE:  2001-03-13
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 126512
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(126512)
;   OTHER INFORMATION: n = A,T,C or G
US-09-804-474A-3

  Query Match          95.7%;  Score 1782.8;  DB 9;  Length 126512;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 1784;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;

Qy         1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2010 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 2069
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Qy      61  TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC  120
            ||||||I.||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2070  TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC  2129

Qy     121  ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2130  ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG  2189

Qy     181  CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2190  CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT  2249

Qy     241  TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2250  TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA  2309

Qy     301  TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2310  TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA  2369

Qy     361  ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC  420
            |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db    2370  ACCAGCACAACAACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC  2429

Qy     421  CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2430  CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC  2489

Qy     481  ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2490  ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC  2549

Qy     541  ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA  600
            ||||||||||||||.|||||||||||||||||||||||||||||||||||||||||||||
Db    2550  ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA  2609

Qy     601  CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2610  CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT  2669

Qy     661  CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2670  CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC  2729

Qy     721  TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2730  TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC  2789

Qy     781  ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC  840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2790  ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC  2849

Qy     841  CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC  900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2850  CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC  2909

Qy     901  CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC  960
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                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2910   CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC   2969

Qy       961   AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT   1020
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2970   AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT   3029

Qy      1021   TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT   1080
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3030   TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT   3089

Qy      1081   ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC   1140
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3090   ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC   3149

Qy      1141   TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT   1200
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3150   TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT   3209

Qy      1201   GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG   1260
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3210   GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG   3269

Qy      1261   AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC   1320
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3270   AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC   3329

Qy      1321   AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC   1380
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3330   AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC   3389

Qy      1381   CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC   1440
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3390   CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC   3449

Qy      1441   TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA   1500
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3450   TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA   3509

Qy      1501   GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA   1560
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3510   GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA   3569

Qy      1561   GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT   1620
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3570   GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT   3629

Qy      1621   GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT   1680
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3630   GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT   3689

Qy      1681   ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT   1740
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3690   ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT   3749

Qy      1741   GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT   1786
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RESULT 9
US-10-114-153-1
; Sequence 1, Application US/10114153
; Publication No. US20030185815A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Heyes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina
; APPLICANT: MacDougall, John
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES,
NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710

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    Query Match            95.7%;   Score 1782.4;   DB 15;   Length 2813;
    Best Local Similarity  99.9%;   Pred. No. 0;
    Matches 1783;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 68

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 128

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 188

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 248

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 308

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 368

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 428

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 488

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 548

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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                III IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Db       549 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 608

Qy       601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
                IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Db       609 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 668

Qy       661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
                IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Db       669 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 728

Qy       721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
                IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Db       729 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 788

Qy       781 ATGCACAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
                IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Db       789 ATGCACAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 848

Qy       841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
                IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Db       849 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 908

Qy       901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
                IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Db       909 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 968

Qy       961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
                IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Db       969 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1028

Qy      1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
                IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII IIIIIIIIIIIIIIIIIIIIIII
Db      1029 TACTATGCTCTTTCCCACCAACAGAAGAGCCGTGCCTTCTACCGTATCCAAGCCACTCGT 1088

Qy      1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
                IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Db      1089 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1148

Qy      1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
                IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Db      1149 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1208

Qy      1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
                IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Db      1209 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1268

Qy      1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
                IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Db      1269 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1328

Qy      1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
                IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Db      1329 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1388

Qy      1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
                IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
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Db     1389  CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1448

Qy     1441  TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1449  TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1508

Qy     1501  GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1509  GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1568

Qy     1561  GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1569  GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1628

Qy     1621  GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1629  GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1688

Qy     1681  ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1689  ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1748

Qy     1741  GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGT 1784
             ||||||||||||||||||||||||||||||||||||||||||||
Db     1749  GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGT 1792
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RESULT 10
US-10-114-153-3
; Sequence 3, Application US/10114153
; Publication No. US20030185815A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Heyes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina
; APPLICANT: MacDougall, John

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   Query Match            95.7%;  Score 1782.4;  DB 15;  Length 2840;
   Best Local Similarity  99.9%;  Pred. No. 0;
   Matches 1783;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;


Qy        1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       63 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 122


Qy       61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      123 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 182


Qy      121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      183 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 242


Qy      181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       243 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 302

Qy       241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       303 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 362

Qy       301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       363 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 422

Qy       361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       423 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 482

Qy       421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       483 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 542

Qy       481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       543 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 602

Qy       541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       603 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 662

Qy       601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       663 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 722

Qy       661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       723 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 782

Qy       721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       783 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 842

Qy       781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       843 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 902

Qy       841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       903 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 962

Qy       901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       963 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1022

Qy       961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1023 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1082

Qy      1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
                    |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
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Db    1083 TACTATGCTCTTTCCCACCAACAGAAGAGCCGTGCCTTCTACCGTATCCAAGCCACTCGT 1142

Qy    1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1143 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1202

Qy    1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1203 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1262

Qy    1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1263 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1322

Qy    1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1323 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1382

Qy    1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1383 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1442

Qy    1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1443 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1502

Qy    1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1503 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1562

Qy    1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1563 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1622

Qy    1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1623 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1682

Qy    1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1683 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1742

Qy    1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1743 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1802

Qy    1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGT 1784
           ||||||||||||||||||||||||||||||||||||||||||||
Db    1803 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGT 1846
```

RESULT 11
US-10-114-153-5

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Query Match              91.0%;   Score 1694.8;   DB 15;   Length 2685;
Best Local Similarity    98.2%;   Pred. No. 0;
Matches 1725;  Conservative    0;  Mismatches   27;  Indels    4;  Gaps    1;
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Qy      86 GAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTT 145
           ||  |  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 GATCCGAGGCTGGTGGCTCAGGGGACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTT 61

Qy     146 CAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTT 205
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 CAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTT 121

Qy     206 CCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCC 265
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     122 CCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCC 181

Qy     266 TTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAG 325
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     182 TTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAG 241

Qy     326 AGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACAACCACTATTCGGGTCT 385
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     242 AGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACAACCACTATTCGGGTCT 301

Qy     386 GGAATGAAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATAC 445
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     302 GGAATGAAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATAC 361

Qy     446 TCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTA 505
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     362 TCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTA 421

Qy     506 CCATTGTAGGGAGTGCAGCCTTCAACATGTTCATCATCATTGGCATCTGTGTCTACGTGA 565
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     422 CCATTGTAGGGAGTGCAGCCTTCAACATGTTCATCATCATTGGCATCTGTGTCTACGTGA 481

Qy     566 TCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTT 625
           |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db     482 TCCCAGACGGAGAGACTCGCAAGATCAAACATCTACGAGTCTTCTTCATCACCGCTGCTT 541

Qy     626 GGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGG 685
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     542 GGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGG 601

Qy     686 TCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCT 745
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     602 TCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCT 661

Qy     746 GGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACA 805
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      662  GGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACA  721

Qy      806  AACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATG  865
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      722  AACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATG  781

Qy      866  GGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGAAG  925
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      782  GGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGAAG  841

Qy      926  TGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCAG  985
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      842  TGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCAG  901

Qy      986  AGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAACAGA  1045
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      902  AGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAACAGA  961

Qy     1046  AGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCC  1105
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      962  AGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCC  1021

Qy     1106  TGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCG  1165
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1022  TGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCG  1081

Qy     1166  ATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGG  1225
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1082  ATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGG  1141

Qy     1226  AGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCA  1285
             |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db     1142  AGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCA  1201

Qy     1286  TGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCA  1345
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1202  TGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCA  1261

Qy     1346  CAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAA  1405
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1262  CAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAA  1321

Qy     1406  TTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCA  1465
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1322  TTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCA  1381

Qy     1466  TAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGC  1525
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1382  TAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGC  1441

Qy     1526  CTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATG  1585
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1442  CTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATG  1501

Qy     1586  CAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGTGTTATGG  1645
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1502  CAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGTGTTATGG  1561
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Qy      1646 AGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACAGTCATCGTCCCCTTTAGGACAG 1705
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1562 AGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACAGTCATCGTCCCCTTTAGGACAG 1621

Qy      1706 TAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAAT 1765
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1622 TAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAAT 1681

Qy      1766 TCAAGAATGATGAAACTGTATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCC 1825
             ||||||||||||||||      |||||  |  ||   |  |  |    ||  |  ||| |||||||||
Db      1682 TCAAGAATGATGAAAC----TGTGAAAACCATAAGGGTTAAAATAGTAGATGAGGAGGAA 1737

Qy      1826 AAGAGGATAGCAGAGA 1841
             |    |    |||||
Db      1738 TACGAAAGGCAAGAGA 1753


RESULT 12
US-10-029-386-20265
; Sequence 20265, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR GENE
;  TITLE OF INVENTION:  EXPRESSION ANALYSIS TWO
;  FILE REFERENCE: AEOMICA-X-2
;  CURRENT APPLICATION NUMBER: US/10/029,386
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 34288
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 20265
;   LENGTH: 823
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AL160191.1
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
;   OTHER INFORMATION: SWISSPROT HIT: P57103, EVALUE 0.00e+00
;   OTHER INFORMATION: EST_HUMAN HIT: BI913344.1, EVALUE 0.00e+00
;   OTHER INFORMATION: NT HIT: gi15147253, EVALUE 0.00e+00
US-10-029-386-20265

  Query Match            44.1%;  Score 821.4;  DB 15;  Length 823;
  Best Local Similarity  99.9%;  Pred. No. 1.6e-259;
  Matches  822;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy       432 TGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTCATTGCTGGTGA 491
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 TGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTCATTGCTGGTGA 60

Qy       492 TCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATCATCATTGGCAT 551
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATCATCATTGGCAT 120

Qy      552 CTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTT 611
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 CTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTT 180

Qy      612 CATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTT 671
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTT 240

Qy      672 CTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTG 731
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 CTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTG 300

Qy      732 TGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAA 791
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 TGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAA 360

Qy      792 GTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGG 851
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGG 420

Qy      852 CATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCT 911
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 CATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCT 480

Qy      912 GGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAA 971
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAA 540

Qy      972 GCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCT 1031
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCT 600

Qy     1032 TTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGG 1091
                    ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db      601 TTCCCACCAACAGAAGAGCCGTGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGG 660

Qy     1092 TGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAG 1151
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 TGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAG 720

Qy     1152 CGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTC 1211
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 CGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTC 780

Qy     1212 TTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTG 1254
                    |||||||||||||||||||||||||||||||||||||||||||
Db      781 TTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTG 823
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RESULT 13
US-09-901-419-1
; Sequence 1, Application US/09901419
; Patent No. US20020069421A1
; GENERAL INFORMATION:

```
  Query Match              43.5%;  Score 810.6;  DB 9;   Length 4087;
  Best Local Similarity   68.5%;  Pred. No. 1.6e-255;
  Matches 1211;  Conservative    0;  Mismatches  519;  Indels   39;  Gaps     5;


Qy        46 TTTGGGCTGGTTACCTTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCA 105
             |||     || | || | |||    || || |  | | |   |   |      |||
Db       307 TTTCACGTGATAGCCATGGTGGCTCTCTTGTTTTCCCATGTGGACCATATAAGTGCTGAG 366


Qy       106 GGGGACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAG 165
                || || || |   ||| | |||| ||   ||| | || || |   |||| |||
Db       367 ACAGAAATGGAAGGAGAAGGCAACGAGACTGGCGAGTGTACTGGCTCCTATTACTGTAAG 426


Qy       166 GAGGGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCC 225
             |||| || ||  |  || || ||| | ||  || ||||||||| |||| ||||| |||||
Db       427 AAGGGGGTGATTTTACCCATTTGGGAGCCCCAGGACCCTTCCTTTGGAGACAAAATTGCT 486


Qy       226 AGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCT 285
             || |   | ||| |||||||||||| || | | ||||||||| ||||| || || |||||||||
Db       487 AGAGCGACTGTGTATTTTGTGGCCATGGTCTACATGTTTCTTGGAGTCTCAATCATTGCT 546


Qy       286 GACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAG 345
             ||||| |||||| | ||||| |||||||||||| |||||||||| ||  | || || |||
Db       547 GACCGGTTCATGTCCTCTATAGAAGTCATCACGTCTCAAGAGAAAGAAATCACCATAAAG 606


Qy       346 AAACCCAATGGAGAAACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAAC 405
             |||||||||||||| |||| ||  || ||| |  || |||||||||| || || ||||||
Db       607 AAACCCAATGGAGAGACCACCAAGACAACTGTGAGGATCTGGAATGAGACAGTGTCCAAC 666


Qy       406 CTGACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTG 465
             |||||| | |||||||||||| || || ||||| ||||| ||||| |||| |||| ||||||
Db       667 CTGACCTTGATGGCCCTGGGGTCTTCAGCTCCAGAGATTCTCCTTTCAGTAATCGAGGTG 726
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Qy    466  TGTGGTCATGGGGTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCC .525
           |||||  |||    |||| ||| || || || || |||    ||||| || ||||||||| ||
Db    727  TGTGGCCATAACTTCACTGCAGGAGACCTTGGCCCTAGCACCATCGTGGGGAGTGCTGCA  786

Qy    526  TTCAACATGTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGC  585
           |||||||||||||||||||||||||| | | |||||| || || |||| || || ||||| |
Db    787  TTCAACATGTTCATCATCATTGCCCTTTGTGTGTATGTCGTCCCGGATGGGGAGACAAGG  846

Qy    586  AAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATC  645
           |||||||||||||| || || |||||  | || || || ||||| |||||||||||| | |
Db    847  AAGATCAAGCATCTGCGTGTGTTCTTTGTGACAGCAGCATGGAGCATCTTTGCCTATACC  906

Qy    646  TGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTC  705
           ||||| || || ||| || | ||| ||||||||| || || |||| ||||||||||| |
Db    907  TGGCTTTACATCATTTTGTCTGTCAGCTCCCCTGGGGTCGTGGAGGTCTGGGAAGGTTTG  966

Qy    706  CTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTG  765
           || ||| |||||||||| || | || ||  | || |||||||||| |    | ||
Db    967  CTTACTTTCTTCTTCTTCCCCATCTGCGTTGTGTTTGCTTGGGTGGCAGACAGGAGGCTT  1026

Qy    766  CTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATA  825
           || || ||||| || |    |||| | ||| || || | | ||| ||  | ||||| || ||
Db    1027 CTGTTTTACAAGTATGTCTACAAGAGGTATCGGGCTGGCAAGCAGAGGGGAATGATTATT  1086

Qy    826  GAGACAGAGGGTGACCACCC---------TAAGGGCATTGAGATGGATGGGAAAATGATG  876
           ||    || || ||| ||      |  |   ||||| ||||||||||||| || |
Db    1087 GAACACGAAGGAGACAGGCCATCTTCCAAGACAGAAATTGAAATGGATGGGAAAGTGGTC  1146

Qy    877  AATTCCCA--------TTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAG------  921
           ||||||||        |||  ||||||| |||||| |      || |    ||
Db    1147 AATTCCCATGTTGACAGTTTCTTAGATGGAGCCCTGGTTCTGGAGGTTGATGAGAGGGAC  1206

Qy    922  ---GAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAA  978
              || |  || ||  || |  |||| |||       |||||||| ||||| || ||||| ||
Db    1207 CAAGATGATGAAGAAGCCAGGCGAGAAATGGCTAGGATTCTGAAGGAACTCAAGCAGAAG  1266

Qy    979  CACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCAC  1038
           || |||||||||| |    |||| ||   |  | | || | |||||||||| |  |     ||
Db    1267 CATCCAGAGAAGGAAATAGAGCAATTAATAGAATTAGCCAATTACCAAGTCTTAAGTCAG  1326

Qy    1039 CAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGC  1098
           || || || || || || || ||||||||| ||||| || ||    ||||||| || ||||||
Db    1327 CAGCAAAAAGTCGAGCGTTTTACCGTATTCAAGCTACCCGCCTGATGACCGGAGCAGGC  1386

Qy    1099 AATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTG  1158
           || ||  | |||| |||||||||||| |||||||| ||| ||   |||||||    |||||
Db    1387 AACATTTTAAAGAGGCATGCAGCAGACCAAGCCAGGAAAGCTGTCAGCATGCATGAGGTC  1446

Qy    1159 CACACCGATGAGCCTG---AGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTAC  1215
           |||| || || | |||   | ||| | ||    ||| |||||||||| | |  |   | ||
Db    1447 AACACGGAAGTGGCTGAAAATGACCCTGTCAGTAAGATCTTCTTTGAACAAGGGACATAT  1506

Qy    1216 CAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATG  1275
           ||||| ||||||||||||||   | ||| |||||| |  | |   | | ||| || || ||
Db    1507 CAGTGTCTGGAGAACTGTGGCACAGTAGCCCTGACCATTATCCGCAGAGGTGGTGATTTG  1566
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Qy   1276 TCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGAC 1335
           | || ||  ||| |||  |||| ||  |||||||||||||||  | ||||||||| ||  ||||
Db   1567 ACCAACACTGTGTTTGTTGACTTCAGAACAGAGGATGGCACAGCCAATGCTGGATCTGAT 1626

Qy   1336 TATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCC 1395
           || || || || || || || || |||||  | ||||| ||  |||||||||||||||  ||
Db   1627 TACGAATTTACCGAAGGAACTGTGGTCTTTAAGCCTGGTGAGACCCAGAAGGAAATCAGA 1686

Qy   1396 GTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGC 1455
           || |||||  ||||||||| ||||| |||||||||||||||||||||  | ||| ||||    | |||
Db   1687 GTTGGCATCATTGATGATGACATCTTTGAGGAGGATGAGAATTTCCTTGTGCATCTCAGC 1746

Qy   1456 AATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGT 1515
           || |||     ||     |||     | || || || || || |     |||            ||||
Db   1747 AACGTCAAAGTATCTTTGGAAGCCTCGGAAGACGGCATCCTGGAAGC---------CAGT 1797

Qy   1516 CTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGAT 1575
           | |  ||   | |  |||  ||| |  |||||| |     ||||| || || || || |||
Db   1798 CATGTCTCTACCCTTGCTTGCCTGGGATCCCCCTCCACTGCCACCGTGACTATTTTTGAT 1857

Qy   1576 GATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATT 1635
           ||||||||||||| ||||||||| |||||||  |           | ||||||| |||||||| |||
Db   1858 GATGACCATGCTGGCATCTTTACTTTTGAGGAACCGGTGACTCATGTGAGTGAGAGCATT 1917

Qy   1636 GGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACAGTCATCGTCCCC 1695
           ||   |  |||||||| ||  |||||| |  | ||||| ||  || || || |  || ||||| |||
Db   1918 GGCATCATGGAGGTGAAAGTTCTGAGAACATCTGGAGCACGTGGAAATGTTATCGTTCCC 1977

Qy   1696 TTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGG 1755
           | || |||  | || ||||| ||||  |||||  ||  |||||||||||||||||| ||
Db   1978 TATAAGACCATTGAGGGGACCGCCAGAGGTGGAGGGGAGGACTTTGAGGACACATGCGGA 2037

Qy   1756 GAGTTGGAATTCAAGAATGATGAAACTGT 1784
           ||| | || ||| ||||||| |||| |||
Db   2038 GAGCTCGAGTTCCAGAATGACGAAATTGT 2066
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RESULT 14
US-09-864-761-16939
; Sequence 16939, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366

  Query Match   42.1%;   Score 785.2; DB 9;   Length 1836;
  Best Local Similarity   68.3%;   Pred. No. 2.3e-247;
  Matches 1166; Conservative   0; Mismatches 503; Indels   39; Gaps   4;

Qy   109 GACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAG 168
              || || | | ||| | | | || ||| | || |||| |||| ||| |

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Db    133 GAAATGGAAGGAGAAGGAAATGAAACTGGTGAATGTACTGGATCATATTACTGTAAGAAA 192

Qy    169 GGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGG 228
          ||  || ||  |||| || ||| | ||  |  |||||||  |||||||||| ||||| ||
Db    193 GGGGTGATTTTGCCCATTTGGGAACCCCAAGACCCTTCTTTTGGGGACAAAATTGCTAGA 252

Qy    229 GTCATTGTCTATTTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGAC 288
          |   | ||| |||||||||||| || | | |||||||| |||||| || || ||||| |||||
Db    253 GCTACTGTGTATTTTGTGGCCATGGTCTACATGTTTCTTGGAGTCTCTATCATAGCTGAT 312

Qy    289 CGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAA 348
          || ||||||| | |||||| ||||||||||||||| |||||||| |  || | || || ||||||
Db    313 CGGTTCATGTCCTCTATAGAAGTCATCACATCTCAAGAAAAAGAAATAACCATAAAGAAA 372

Qy    349 CCCAATGGAGAAACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTG 408
          |||||||||| |||| || || ||| |  || ||||||||||||||| || || ||||||
Db    373 CCCAATGGAGAGACCACCAAGACAACTGTGAGGATCTGGAATGAAACAGTTTCTAACCTG 432

Qy    409 ACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGT 468
          ||| | |||||||||||| || |||||||||||| || ||| ||||||| ||||||
Db    433 ACCTTGATGGCCCTGGGATCTTCTGCTCCTGAGATTCTCCTTTCAGTAATTGAAGTGTGT 492

Qy    469 GGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTC 528
          || |||    |||| ||| || || || || || |||    ||||| || || ||||| || |||
Db    493 GGCCATAACTTCACTGCAGGAGACCTCGGTCCTAGCACCATCGTGGGAAGTGCTGCATTC 552

Qy    529 AACATGTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAG 588
          || |||||||||||| ||||    ||||||| || ||| | || |||||||||||  | |||
Db    553 AATATGTTCATCATTATTGCACTCTGTGTTTATGTGGTGCCTGACGGAGAGACAAGGAAG 612

Qy    589 ATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGG 648
          || |||||| | || |||||||| | || || || ||||| |||||||||||||||| ||||
Db    613 ATTAAGCATTTGCGTGTCTTCTTTGTGACAGCAGCCTGGAGCATCTTTGCCTACACCTGG 672

Qy    649 CTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTC 708
          || || || ||| || | ||| | || ||||||||| || |||| ||||||||| | ||
Db    673 CTTTACATTATTTTGTCTGTCATATCTCCTGGTGTTGTGGAGGTCTGGGAAGGTTTGCTT 732

Qy    709 ACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTC 768
          ||| |||||||||||||||| | |||||| |  | || ||||| || |||| |||| ||
Db    733 ACTTTCTTCTTCTTTCCCATCTGTGTTGTGTTCGCTTGGGTAGCGGATAGGAGACTTCTG 792

Qy    769 TTCTACAAATACATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAG 828
          || ||||| || | | |||| | ||| || | | |||| || | || || || || || ||
Db    793 TTTTACAAGTATGTCTACAAGAGGTATCGAGCTGGCAAGCAGAGGGGGATGATTATTGAA 852

Qy    829 ACAGAGGGTGACCACCC---------TAAGGGCATTGAGATGGATGGGAAAATGATGAAT 879
          ||  || ||| ||    ||             | |  | ||||| ||||| |||||| | | |||
Db    853 CATGAAGGAGACAGGCCATCTTCTAAGACTGAAATTGAAATGGACGGGAAAGTGGTCAAT 912

Qy    880 TCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAG------------------ 921
          || ||| || | ||     |  | |||| |      | |||||     | ||
Db    913 TCTCATGTTGAAAATTTCTTAGATGGTGCTCTGGTTCTGGAGGTGGATGAGAGGGACCAA 972

Qy    922 GAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACAC 981
          || |  || || || |  |  | |||| ||| |||||||| |||||| || ||||| || ||
Db    973 GATGATGAAGAAGCTAGGCGAGAAATGGCTAGGATTCTGAAGGAACTTAAGCAGAAGCAT 1032
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Qy    982 CCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAA 1041
          ||||| || ||  |||| ||  |  | ||  | || || ||| | |  ||    || ||
Db   1033 CCAGATAAAGAAATAGAGCAATTAATAGAATTAGCTAACTACCAAGTCCTAAGTCAGCAG 1092

Qy   1042 CAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAAT 1101
          || || ||  | | || || || || || ||||| ||||| | |||||||| || |||||
Db   1093 CAAAAAGTAGAGCATTTTATCGCATTCAAGCTACTCGCCTCATGACTGGAGCTGGCAAC 1152

Qy   1102 ATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCAC 1161
          ||  | ||||  ||||||| |||||| || |||||| | |||||||   ||||||| ||||  ||
Db   1153 ATTTTAAAGAGGCATGCAGCTGACCAAGCAAGGAAGGCTGTCAGCATGCACGAGGTCAAC 1212

Qy   1162 ACCGATGAGCCTG---AGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAG 1218
          || || | ||| | |||  | ||  |||  |||||||||| | | | |  | ||| |||
Db   1213 ACTGAAGTGACTGAAAATGACCCTGTTAGTAAGATCTTCTTTGAACAAGGGACATATCAG 1272

Qy   1219 TGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCA 1278
          ||  ||||||||||||| || ||    |||| || ||  |  |  | ||| || ||  || |
Db   1273 TGTCTGGAGAACTGTGGTACTGTGGCCCTTACCATTATCCGCAGAGGTGGTGATTTGACT 1332

Qy   1279 AAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTAT 1338
          || ||   ||| ||| |||| || ||||||||||||   |  || ||||| ||| ||| |||
Db   1333 AACACTGTGTTTGTTGACTTCAGAACAGAGGATGGCACAGCAAATGCTGGGTCTGATTAT 1392

Qy   1339 GAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTG 1398
          || || || || || || || || ||||| | ||||| || || |||||||||||| |||
Db   1393 GAATTTACTGAAGGAACTGTGGTGTTTAAGCCTGGTGATACCCAGAAGGAAATCAGAGTG 1452

Qy   1399 GGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAAT 1458
          || || || ||||| || || ||||||||||||||||| | ||| |||   | ||||||
Db   1453 GGTATCATAGATGATGATATCTTTGAGGAGGATGAAAATTTCCTTGTGCATCTCAGCAAT 1512

Qy   1459 GTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTT 1518
          ||   ||  ||      | | ||||  ||  || || ||  | |||       || || |
Db   1513 GTCAAAGTATCTTCTGAAGCTTCAGAAGATGGCATACTGGAAGC---------CAATCAT 1563

Qy   1519 CCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGAT 1578
          | | | | ||| ||| | ||||| | |  ||||| || || || || || |||||||
Db   1564 GTTTCTACACTTGCTTGCCTCGGATCTCCCTCCACTGCCACTGTAACTATTTTTGATGAT 1623

Qy   1579 GACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGT 1638
          ||||| |||||||| |||| ||||||| |    |  | |||||| ||||||||| |||||
Db   1624 GACCACGCAGGCATTTTTACTTTTGAGGAACCTGTGACTCATGTGAGTGAGAGCATTGGC 1683

Qy   1639 GTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACAGTCATCGTCCCCTTT 1698
          | |||||||| ||| || || || ||||| || || || || || | || |||||| | |
Db   1684 ATCATGGAGGTGAAAGTATTGAGAACATCTGGAGCTCGAGGAAATGTTATCGTTCCATAT 1743

Qy   1699 AGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAG 1758
          | || | ||||||||| || |||||| || || || ||||| ||||| |||||| || |||
Db   1744 AAAACCATCGAAGGGACTGCCAGAGGTGGAGGGGAGGATTTTGAGGACACTTGTGGAGAG 1803

Qy   1759 TTGGAATTCAAGAATGATGAAACTGTAT 1786
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Db   1804 CTCGAATTCCAGAATGATGAAATTGTGT 1831
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RESULT 15
US-10-062-674-1648
; Sequence 1648, Application US/10062674
; Publication No. US20040005559A1
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.
; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
; FILE REFERENCE: PA-0026-1 CIP
; CURRENT APPLICATION NUMBER: US/10/062,674
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: US 09/625,102
; PRIOR FILING DATE: 2000-07-24
; NUMBER OF SEQ ID NOS: 2217
; SOFTWARE: PERL Program
; SEQ ID NO 1648
;   LENGTH: 6106
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20040005559A1 221501.2
US-10-062-674-1648

  Query Match   42.0%;   Score 783.2; DB 16; Length 6106;
  Best Local Similarity   68.2%;   Pred. No. 2.3e-246;
  Matches 1164; Conservative   0; Mismatches 503; Indels   39; Gaps   4;

Qy   109 GACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAG 168
              || || | | ||| | | || || ||| | || ||| |||| ||| |
Db   192 GAAATGGAAGGAGAAGGAAATGAAACTGGTGAATGTACTGGATCATATTACTGTAAGAAA 251

Qy   169 GGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGG 228
              || || || |||| || ||| | || | ||||||| |||||||||| ||||| ||
Db   252 GGGGTGATTTTGCCCATTTGGGAACCCCAAGACCCTTCTTTTGGGGACAAAATTGCTAGA 311

Qy   229 GTCATTGTCTATTTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGAC 288
              | | ||| ||||||||||||| || | |||||||| ||||| || || ||||| |||||
Db   312 GCTACTGTGTATTTTGTGGCCATGGTCTACATGTTTCTTGGAGTCTCTATCATAGCTGAT 371

Qy   289 CGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAA 348
              || ||||||| | ||||| |||||||||||| | || || | || || ||||||
Db   372 CGGTTCATGTCCTCTATAGAAGTCATCACATCTCAAAAAAAAGAAATAACCATAAAGAAA 431

Qy   349 CCCAATGGAGAAACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTG 408
              |||||||||| |||| || || ||| | || ||||||||||||| || || ||||||
Db   432 CCCAATGGAGAGACCACCAAGACAACTGTGAGGATCTGGAATGAAACAGTTTCTAACCTG 491

Qy   409 ACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGT 468
              ||| | ||||||||||| || |||||||||||||| |||||| || |||||| ||||||
Db   492 ACCTTGATGGCCCTGGGGATCTTCTGCTCCTGAGATTCTCCTTTCAGTAATTGAAGTGTGT 551

Qy   469 GGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTC 528
              || ||| |||| ||| || || || || || ||||| || || |||||| || |||
Db   552 GGCCATAACTTCACTGCAGGAGACCTCGGTCCTAGCACCATCGTGGGAAGTGCTGCATTC 611

Qy   529 AACATGTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAG 588

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Db    612 AATATGTTCATCATTATTGCACTCTGTGTTTATGTGGTGCCTGACGGAGAGACAAGGAAG 671

Qy    589 ATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGG 648
                     ||  |||||||  |  ||  |||||||||   |  ||  ||  ||  ||||||  |||||||||||||||  ||||
Db    672 ATTAAGCATTTGCGTGTCTTCTTTGTGACAGCAGCCTGGAGCATCTTTGCCTACACCTGG 731

Qy    649 CTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTC 708
                     ||  ||  ||  |||  ||  |  |||  |  ||  ||||||||  ||    ||||  ||||||||   |  ||
Db    732 CTTTACATTATTTTGTCTGTCATATCTCCTGGTGTTGTGGAGGTCTGGGAAGGTTTGCTT 791

Qy    709 ACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTC 768
                     |||  ||||||||||||||  |  |||||  |  |  ||  |||||  ||  ||||     ||||  ||
Db    792 ACTTTCTTCTTCTTTCCCATCTGTGTTGTGTTCGCTTGGGTAGCGGATAGGAGACTTCTG 851

Qy    769 TTCTACAAATACATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAG 828
                     ||  ||||||  ||   |   ||||| |  |||   |  |  |||  ||   |  ||  ||  ||  ||  ||
Db    852 TTTTACAAGTATGTCTACAAGAGGTATCGAGCTGGCAAGCAGAGGGGGATGATTATTGAA 911

Qy    829 ACAGAGGGTGACCACCC---------TAAGGGCATTGAGATGGATGGGAAAATGATGAAT 879
                     ||  ||  |||    ||        |  |   |||||  |||||  ||||||  ||  |  |||
Db    912 CATGAAGGAGACAGGCCATCTTCTAAGACTGAAATTGAAATGGACGGGAAAGTGGTCAAT 971

Qy    880 TCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAG------------------ 921
                     ||  |||  ||   |  ||       |   |  |||||     |  |||
Db    972 TCTCATGTTGAAAATTTCTTAGATGGTGCTCTGGTTCTGGAGGTGGATGAGAGGGACCAA 1031

Qy    922 GAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACAC 981
                     ||  |  ||  ||  |  |  ||||  |||     |||||||  |||||  ||  |||||||  ||  ||
Db   1032 GATGATGAAGAAGCTAGGCGAGAAATGGCTAGGATTCTGAAGGAACTTAAGCAGAAGCAT 1091

Qy    982 CCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAA 1041
                     |||||  ||  ||   ||||  ||  |  |  ||  |  ||  ||  |||  |  |  ||     ||  ||
Db   1092 CCAGATAAAGAAATAGAGCAATTAATAGAATTAGCTAACTACCAAGTCCTAAGTCAGCAG 1151

Qy   1042 CAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAAT 1101
                     ||  ||  ||   |  ||  ||  ||  ||  ||  |||||  |||||     |  |||||||  ||  |||||
Db   1152 CAAAAAAGTAGAGCATTTTATCGCATTCAAGCTACTCGCCTCATGACTGGAGCTGGCAAC 1211

Qy   1102 ATCCTGAAGAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCAC 1161
                     ||  |  ||||  |||||||||.||  ||||||  |  ||||||     |||||||  ||||||  ||
Db   1212 ATTTTAAAGAGGCATGCAGCTGACCAAGCAAGGAAGGCTGTCAGCATGCACGAGGTCAAC 1271

Qy   1162 ACCGATGAGCCTG---AGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAG 1218
                     ||  ||  |  |||     |  |||  |  ||     |||  |||||||||||  |  |  |  |||
Db   1272 ACTGAAGTGACTGAAAATGACCCTGTTAGTAAGATCTTCTTTGAACAAGGGACATATCAG 1331

Qy   1219 TGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCA 1278
                     ||  ||||||||||||||||||||    ||||     |||  ||   |  |  |  ||  |||  ||  ||     ||  |
Db   1332 TGTCTGGAGAACTGTGGTACTGTGGCCCTTACCATTATCCGCAGAGGTGGTGATTTGACT 1391

Qy   1279 AAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTAT 1338
                     ||  ||   |||  |||  ||||  ||  |||||||||||||  |  ||  ||||||  |||  ||||  |||
Db   1392 AACACTGTGTTTGTTGACTTCAGAACAGAGGATGGCACAGCAAATGCTGGGTCTGATTAT 1451

Qy   1339 GAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTG 1398
                     ||  ||  ||  ||  ||  ||  ||  |||||   |  |||||  ||  ||  ||||||||||||  ||     |||
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Db   1452 GAATTTACTGAAGGAACTGTGGTGTTTAAGCCTGGTGATACCCAGAAGGAAATCAGAGTG 1511

Qy   1399 GGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAAT 1458
               || || || ||||| || || |||||||||||||||| | ||| ||||     | ||||||
Db   1512 GGTATCATAGATGATGATATCTTTGAGGAGGATGAAAATTTCCTTGTGCATCTCAGCAAT 1571

Qy   1459 GTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTT 1518
               |||    ||      ||     |||| || || || |    |||          || || |
Db   1572 GTCAAAGTATCTTCTGAAGCTTCAGAAGATGGCATACTGGAAGC---------CAATCAT 1622

Qy   1519 CCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGAT 1578
               |    | | ||| ||| | || || |     |||||| || || || || ||||||
Db   1623 GTTTCTACACTTGCTTGCCTCGGATCTCCCTCCACTGCCACTGTAACTATTTTTGATGAT 1682

Qy   1579 GACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGT 1638
               ||||| |||||||| || ||||||||       |  | ||||||| ||||||||| |||||
Db   1683 GACCACGCAGGCATTTTTACTTTTGAGGAACCTGTGACTCATGTGAGTGAGAGCATTGGC 1742

Qy   1639 GTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACAGTCATCGTCCCCTTT 1698
               | ||||||||| || || || | ||||| || || || || | || ||||| || | |
Db   1743 ATCATGGAGGTGAAAGTATTGAGAACATCTGGAGCTCGAGGAAATGTTATCGTTCCATAT 1802

Qy   1699 AGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAG 1758
               | || | |||||||| |||| ||||| || ||||| ||||| ||||| | ||| |||
Db   1803 AAAACCATCGAAGGGACTGCCAGAGGTGGAGGGGAGGATTTTGAGGACACTTGTGGAGAG 1862

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Db   1863 CTCGAATTCCAGAATGATGAAATTGT 1888
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Job time : 760.008 secs